

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: November 25, 2003, 22:28:25 ; Search time 5208.63 Seconds
(without alignments)
16556.656 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
Searched: 2888711 seqs, 2045481386 residues
Total number of hits satisfying chosen parameters: 5777422
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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7	1979.4	93.9	3007	6	AX234498	AX234498 Sequence
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42	283.4	13.4	289	6	AX027970	AX027970 Sequence
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ALIGNMENTS

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LOCUS AF244813
DEFINITION Homo sapiens platelet-derived growth factor C mRNA, complete cds.
ACCESSION AF244813
VERSION AF244813.1 GI:8886883
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2152)
AUTHORS Li,X., Ponten,A., Aase,K., Karlsson,L., Abramson,A., Utela,M., Backstrom,G., Hellstrom,M., Bostrom,H., Li,H., Soriano,P., Betscholtz,C., Heidin,C.-H., Alitalo,K., Ostman,A. and Eriksson,U.

TITLE PDGF-C is a new protease-activated ligand for the PDGF
 JOURNAL alpha-receptor
 MEDLINE Nat. Cell Biol. 2 (5), 302-309 (2000)
 PUBMED 20262201
 REFERENCE 2 (bases 1 to 2152)
 AUTHORS Eriksson, U., Aase, K., Li, X. and Ponten, A.
 TITLE Direct Submission
 JOURNAL Submitted (14-MAR-2000) Ludwig Institute for Cancer Research,
 Nobels vag 3 P.O. Box 240, Stockholm S-171 77, Sweden
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 Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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AR210624 LOCUS 2825 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 1 from patent US 6391311.
ACCESSION AR210624
VERSION AR210624.1 GI:21513401
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Ferrara, N. and Kuo, S. S.
TITLE Polypeptides having homology to vascular endothelial cell growth
factor and bone morphogenetic protein 1
JOURNAL Patent: US 6391311-A 1 21-MAY-2002;
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RESULT 3
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KEYWORDS
Unknown.
SOURCE
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ORGANISM
Unclassified.
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1 (bases 1 to 2825)
AUTHORS
Ferrara, N. and Kuo, S.S.
TITLE
Nucleic acids encoding vascular endothelial cell growth factor-E
JOURNAL
Patent: US 6455283-A 1. 24-SEP-2002;
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Best Local Similarity 97.7%; Pred. No. 0;
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DB 1028 ACAATTGCAATGAATGTCAATGTGCCCAAGCAAGTACTTAAAAAATACCAAGAGTCC 1087

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DB 1088 TTCAGTTGAGACCAAGACCGGTGTCCAGGGATTCACAAATCCTCACCGAGTGGCCC 1147

QY 1022 TGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGAGGACACAGGAGTATGCCGATC 1081
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DEFINITION Sequence 32 from patent US 6495668.
ACCESSION AR267280
VERSION AR267280.1 GI:29697283
KEYWORDS Unknown.

Wed Nov 26 13:03:28 2003

ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 1760)
TITLE	Gilbert, T., Hart, C.E., Sheppard, P.O. and Gilbertson, D.G.
JOURNAL	Growth factor homolog zveg34
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Best Local Similarity	99.7%; Pred. No. 0;
Matches 1637; Conservative	1; Mismatches 3; Indels 1; Gaps 1;
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Db	1019 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAGATTACTAAAAATACCAAGAGTCC 1078
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DEFINITION	Sequence 1 from patent US 6528050.
ACCESSION	AR282949
VERSION	AR282949.1
KEYWORDS	GI:29719770
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 1760)
TITLE	Gao, Z., Hart, C.E., Piddington, C.S., Sheppard, P.O., Shoemaker, K.E.,
JOURNAL	Gilbertson, D.G. and West, J.W.
FEATURES	Growth factor homolog zveg3 Patent: US 6528050-A 1 04-MAR-2003; Location/Qualifiers 1..1760

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BASE COUNT 494 a 373 c 411 g 482 t

ORIGIN

Query Match 77.1%; Score 1624.8; DB 6; Length 1760;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1637; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

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VERSION AX118785.1 GI:14035734
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ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gilbertson, D. G.
TITLE Method of treating fibrosis
JOURNAL Patent: WO 0128586-A 1 26-APR-2001;
ZymoGenetics, Inc. (US)
FEATURES Location/Qualifiers
source 1. 1760

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BASE COUNT 494 a 373 c 411 g 482 t
ORIGIN
Query Match 77.1%; Score 1624.8; DB 6; Length 1760;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1637; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
QY 2 CCGCGCGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCTCG 61
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DEFINITION complete cds.

ACCESSION AB033831

VERSION AB033831.1 GI:9392293

KEYWORDS spinal cord-derived growth factor; scdGF gene.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

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us-09-852-209a-2.rge

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Job time : 5217.63 secs

GenCore version 5.1.6
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QM nucleic - nucleic search, using sw model

Run on: November 25, 2003, 22:26:15 ; Search time 389.226 Seconds
(without alignments)
14619.814 Million cell updates/sec

Title: US-09-852-209A-2

Perfect score: 2108

Sequence: 1 cccgcgcgtgagtgactct.....nctttttgaaataattaa 2108

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_19Jun03.*

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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2103.6	99.8	2108	21	AAA12523
2	1979.4	93.9	2825	20	AAZ23691
3	1979.4	93.9	2825	25	ABSS7294
4	1979.4	93.9	2839	21	AAA47452
5	1979.4	93.9	2849	20	AAZ34296
6	1979.4	93.9	2849	21	AAC78582
7	1979.4	93.9	2849	21	AAA88515
8	1979.4	93.9	2849	21	AAC58579

XX	Key	Location/Qualifiers
XX	CDS	37..1073
XX	FT	/*tag= a
XX	FT	/product= "platelet-derived growth factor C"
XX	XX	WO200018212-A2.
XX	XX	06-APR-2000.
XX	XX	30-SEP-1999; 99W-US23668.
XX	XX	30-SEP-1998; 98US-0102461.
XX	XX	12-NOV-1998; 98US-0108109.

ALIGNMENTS

RESULT 1

AAA12523

ID AAA12523 standard; cDNA; 2108 BP.

XX

AC AAA12523;

XX

DT 25-JUL-2000 (first entry)

XX

DE cDNA encoding platelet-derived growth factor C (PDGF-C).

XX

KW Platelet-derived growth factor C; PDGF-C; cell proliferation;

KW growth factor; heparin; connective tissue; wound healing; VEGF-F;

KW fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;

KW choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia;

KW lung carcinoma; erythroleukemia; tissue remodelling; ss.

XX

OS Homo sapiens.

XX

XX Key

XX Location/Qualifiers

XX CDS

XX 37..1073

XX /*tag= a

XX /product= "platelet-derived growth factor C"

XX

XX WO200018212-A2.

XX

XX 06-APR-2000.

XX

XX 30-SEP-1999; 99W-US23668.

XX

XX 30-SEP-1998; 98US-0102461.

XX

XX 12-NOV-1998; 98US-0108109.

XX

XX

XX

XX

PR 03-DEC-1998; 98US-0110749.
 PR 18-DEC-1998; 98US-0113002.
 PR 21-MAY-1999; 99US-0135426.
 PR 15-JUN-1999; 99US-0144022.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (UYHE-) UNIV HELSINKI LICENSING LTD.
 XX Eriksson U, Aase K, Lee X, Ponten A, Uutela M, Alitalo K;
 PI Oestman A, Heldin C, Betscholz C;
 XX WPI; 2000-292954/25.
 DR P-PSDB; AAY84557.
 XX Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,
 PT differentiation, growth and motility of cells expressing the PDGF-C
 PT receptor -
 XX Claim 9; Fig 1; 135pp; English.
 PS The present sequence encodes human platelet-derived growth factor C
 CC (PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the
 CC ability to stimulate and enhance proliferation or differentiation,
 CC and/or growth or motility of cells expressing a PDGF-C receptor.
 CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell
 CC proliferation, preferably in combination with one other growth factor
 CC and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also
 CC be used for stimulating connective tissue or wound healing. The
 CC PDGF-C polypeptide can be enzymatically processed to generate the active
 CC truncated form of PDGF-C and used to regulate the receptor-binding
 CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
 CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.
 CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour
 CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
 CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
 CC and erythroleukemia, can be identified by testing for expression of
 CC PDGF-C. PDGF-C antagonists can also be used to inhibit tissue
 CC remodelling during invasion of tumour cells into a normal population of
 CC cells. Antagonists can also be used to treat fibrotic conditions,
 CC especially found in the lung, kidney or liver.
 XX
 SQ Sequence 2108 BP; 623 A; 400 C; 451 G; 629 T; 5 other;

Query Match 99.8%; Score 2103.6; DB 21; Length 2108;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGCCGTGAGTGAGCTCTACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCCTCG 60
 DB 1 CCCGCCGTGAGTGAGCTCTACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCCTCG 60

QY 61 GTGACATCTGCCCTGGCCGGCCAGAGACGAGGACTCAGGGCGGAATCCAACTGAGTAGT 120
 DB 61 GTGACATCTGCCCTGGCCGGCCAGAGACGAGGACTCAGGGCGGAATCCAACTGAGTAGT 120

QY 121 AAATTCAGATTTCCAGCAACAGAGACAGACGAGATCAAGATCCTCAGCATGAGAGA 180
 DB 121 AAATTCAGATTTCCAGCAACAGAGACAGACGAGATCAAGATCCTCAGCATGAGAGA 180

QY 181 ATTATTACTGTCTACTAAATGGAAGTATTACAGCCCAAGGTTTCCTCATCTTATCCA 240
 DB 181 ATTATTACTGTCTACTAAATGGAAGTATTACAGCCCAAGGTTTCCTCATCTTATCCA 240

QY 241 AGAATACGGTCTTGGTATGAGATTTAGTAGCAGTAGAGGAAAATGTATGGATACAATT 300
 DB 241 AGAATACGGTCTTGGTATGAGATTTAGTAGCAGTAGAGGAAAATGTATGGATACAATT 300

QY 301 AGTTTGTATGAAGATTTGGGCTTGAAGCCAGAGATGACATATGCAAGTATGATTT 360
 DB 301 AGTTTGTATGAAGATTTGGGCTTGAAGCCAGAGATGACATATGCAAGTATGATTT 360

QY 361 GTAGAAGTTGAGAAACCCAGTGATGGAACATATATTAGGCGCTGTGTGTTCTCGTACT 420
 DB 361 GTAGAAGTTGAGAAACCCAGTGATGGAACATATATTAGGCGCTGTGTGTTCTCGTACT 420

DB 361 GTAGAAGTTGAGAAACCCAGTGATGGAACATATATTAGGCGCTGTGTGTTCTCGTACT 420
 QY 421 GTACAGGAAAACAGATTTCTTAAAGGAATCAAATTAGGATAAGATTTGTATCTCATGAA 480
 DB 421 GTACAGGAAAACAGATTTCTTAAAGGAATCAAATTAGGATAAGATTTGTATCTCATGAA 480
 QY 481 TATTTCTCTCTGAAACCAAGGTTCTGCATCCACTACAAACATTTGTCTCATGCAATTCACA 540
 DB 481 TATTTCTCTCTGAAACCAAGGTTCTGCATCCACTACAAACATTTGTCTCATGCAATTCACA 540
 QY 541 GAAGCTGTGAGTCTTCTAGTCTACCCCTTTCAGCTTTGGCCACTGGACCTGCTTAAATAT 600
 DB 541 GAAGCTGTGAGTCTTCTAGTCTACCCCTTTCAGCTTTGGCCACTGGACCTGCTTAAATAT 600
 QY 601 GCTATAACTGCTTTAGTACCTTTGGAAGACCTTATTCGATATCTTTGAAACAGAGAGATGG 660
 DB 601 GCTATAACTGCTTTAGTACCTTTGGAAGACCTTATTCGATATCTTTGAAACAGAGAGATGG 660
 QY 661 CAGTTGGAATTTAGAGATCTATATAGGCCAACTTGGCAACTTCTTTGGCAAGGCTTTTGT 720
 DB 661 CAGTTGGAATTTAGAGATCTATATAGGCCAACTTGGCAACTTCTTTGGCAAGGCTTTTGT 720
 QY 721 TTTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTTAAACAGAGAGGTAAAGATTATAC 780
 DB 721 TTTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTTAAACAGAGAGGTAAAGATTATAC 780
 QY 781 AGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGGGAAGAACTAAAGAGAACCGATACC 840
 DB 781 AGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGGGAAGAACTAAAGAGAACCGATACC 840
 QY 841 ATTTTCTGGCAGGTTGTCTCTCTGTTTAAACGCTGTGTGGGAACTGTGCTGTTGTCTC 900
 DB 841 ATTTTCTGGCAGGTTGTCTCTCTGTTTAAACGCTGTGTGGGAACTGTGCTGTTGTCTC 900
 QY 901 CACAAATTCGAATGATGTCCTCAAGCAAGTCTTCTTAAATAATACCAACGAGTCTC 960
 DB 901 CACAAATTCGAATGATGTCCTCAAGCAAGTCTTCTTAAATAATACCAACGAGTCTC 960
 QY 961 CTTCAAGTTGAGACCAAGAACCGGCTCAGGGGATTCGCAAAATCACTCACCGACGTGGCC 1020
 DB 961 CTTCAAGTTGAGACCAAGAACCGGCTCAGGGGATTCGCAAAATCACTCACCGACGTGGCC 1020

QY 1021 CTGAGGACCAATGAGGAGTGTGATCTGTGTGTCAGAGGAGACACAGGAGGATAGCGGAT 1080
 DB 1021 CTGAGGACCAATGAGGAGTGTGATCTGTGTGTCAGAGGAGACACAGGAGGATAGCGGAT 1080

QY 1081 CACCAACAGCAGCTCTTCCAGAGCTGTGCAGTGCAGTGGCTGATTTCTATTAGAGAACG 1140
 DB 1081 CACCAACAGCAGCTCTTCCAGAGCTGTGCAGTGCAGTGGCTGATTTCTATTAGAGAACG 1140

QY 1141 TATCGTTTATCTCCATCTTAACTTCACTTGTGTTTCTTCAAGGACCTTTTCATCTTCAGGA 1200
 DB 1141 TATCGTTTATCTCCATCTTAACTTCACTTGTGTTTCTTCAAGGACCTTTTCATCTTCAGGA 1200

QY 1201 TTTACAGTGCATCTTGAAGAGGAGACATCAAAAGAAATAGGAGTGTGTGCAACAGCTCT 1260
 DB 1201 TTTACAGTGCATCTTGAAGAGGAGACATCAAAAGAAATAGGAGTGTGTGCAACAGCTCT 1260

QY 1261 TTTGAGAGGAGGCTTAAAGGACAGGAGAAAGGCTTCAATCGTGGAAAGAAATTAAT 1320
 DB 1261 TTTGAGAGGAGGCTTAAAGGACAGGAGAAAGGCTTCAATCGTGGAAAGAAATTAAT 1320

QY 1321 GTTGTATTAAATAGATCAACAGTGTTCAGAGTTTACCATGTATTCACCTAGCTG 1380
 DB 1321 GTTGTATTAAATAGATCAACAGTGTTCAGAGTTTACCATGTATTCACCTAGCTG 1380

QY 1381 GGTCTGTATTTCAGTCTTTCGATACCGCTTATAGGTTAATGTCAAGAGAAAAAACT 1440
 DB 1381 GGTCTGTATTTCAGTCTTTCGATACCGCTTATAGGTTAATGTCAAGAGAAAAAACT 1440

QY 1441 GTGCAAGTGAGCACCTGATTCGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1500
 DB 1441 GTGCAAGTGAGCACCTGATTCGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1500

Db 524 CGTTTGATGAAGATTGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTG 583
QY 362 TAGAAGTTGAGGAACCCAGTATGGAACCTATATAGGGCGCTGGTGGTTCTGGTACTG 421
Db 584 TAGAAGTTGAGGAACCCAGTATGGAACCTATATAGGGCGCTGGTGGTTCTGGTACTG 643
QY 422 TACCAGGAAACAGATTCTTAAAGGAATCAAAATTAGGATAAGATTGTTATCTGATGAAT 481
Db 644 TACCAGGAAACAGATTCTTAAAGGAATCAAAATTAGGATAAGATTGTTATCTGATGAAT 703
QY 482 ATTTTCTCTTGAACAGGGTTCTGATCCACTACCAATTTGTCATGCCCAATTTACAG 541
Db 704 ATTTTCTCTTGAACAGGGTTCTGATCCACTACCAATTTGTCATGCCCAATTTACAG 763
QY 542 AAGCTGTGAGTCTCTGAGTCTACCCCTTTCAGCTTTGCCACTGGACCTGCTTAAATAATG 601
Db 764 AAGCTGTGAGTCTCTGAGTCTACCCCTTTCAGCTTTGCCACTGGACCTGCTTAAATAATG 823
QY 602 CTATAACTGCTTTTGTAGTACTCTTGGAGACCTTATTCGATATCTTGAACAGAGATGGC 661
Db 824 CTATAACTGCTTTTGTAGTACTCTTGGAGACCTTATTCGATATCTTGAACAGAGATGGC 883
QY 662 AGTTGAGCTTAGAGATCTATATAGGCCAACTTTGGCAACTCTTGGCAAGGCTTTTGT 721
Db 884 AGTTGAGCTTAGAGATCTATATAGGCCAACTTTGGCAACTCTTGGCAAGGCTTTTGT 943
QY 722 TTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGAGGTAAAGATTATACA 781
Db 944 TTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGAGGTAAAGATTATACA 1003
QY 782 GCTGCAACCTCTGTAATCTTCTAGTCTCATATAGGGAAGAACTAAAGAGAACCGATCCA 841
Db 1004 GCTGCAACCTCTGTAATCTTCTAGTCTCATATAGGGAAGAACTAAAGAGAACCGATCCA 1063
QY 842 TTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTGGTGGAACTGTGCTGTGCTCTCC 901
Db 1064 TTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTGGTGGAACTGTGCTGTGCTCTCC 1123
QY 902 ACAATTGCAATGTAATGTGTCCCAAGCAAGTTACTAAAAATACCAAGAGTCC 961
Db 1124 ACAATTGCAATGTAATGTGTCCCAAGCAAGTTACTAAAAATACCAAGAGTCC 1183
QY 962 TTCAGTTGAGACCAAGACCGGTGTGAGGGATTTGCAAAATCACTACCGAGTGGCCC 1021
Db 1184 TTCAGTTGAGACCAAGACCGGTGTGAGGGATTTGCAAAATCACTACCGAGTGGCCC 1243
QY 1022 TGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGGATACCCGATC 1081
Db 1244 TGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGGATACCCGATC 1303
QY 1082 ACCACAGACGCTCTTGGCCAGAGCTGTGAGTGTGAGTGTGCTATTTAGAGAACGT 1141
Db 1304 ACCACAGACGCTCTTGGCCAGAGCTGTGAGTGTGAGTGTGCTATTTAGAGAACGT 1363
QY 1142 ATGCGTTATCTCATCTCTAACTCTAGTTGTTTCTTCAAGGACCTTCTATCTTCAGGAT 1201
Db 1364 ATGCGTTATCTCATCTCTAACTCTAGTTGTTTCTTCAAGGACCTTCTATCTTCAGGAT 1423
QY 1202 TTACAGTGTGATCTGAAAGAGGAGACATCAAAAGAAATTAGGAGTTGTGCAACAGCTCTT 1261
Db 1424 TTACAGTGTGATCTGAAAGAGGAGACATCAAAAGAAATTAGGAGTTGTGCAACAGCTCTT 1483
QY 1262 TTGAGAGGAGGCTTAAAGACAGGAGAAAGGTTCTCAATCGTGGAAAGAAATTAATG 1321
Db 1484 TTGAGAGGAGGCTTAAAGACAGGAGAAAGGTTCTCAATCGTGGAAAGAAATTAATG 1543
QY 1322 TTGTATTAATAGATCACAGCTAGTTTTCAGAGTTACCATGTACGTAATCCACTAGCTGG 1381
Db 1544 TTGTATTAATAGATCACAGCTAGTTTTCAGAGTTACCATGTACGTAATCCACTAGCTGG 1603
QY 1382 GTTCTGTATTTTCAAGTTCTTTTCGATACGGCTTAGGGTAAATGTGATGACAGGAAAAAATG 1441
Db 1604 GTTCTGTATTTTCAAGTTCTTTTCGATACGGCTTAGGGTAAATGTGATGACAGGAAAAAATG 1663

QY 1442 TGCAAGTGAACCTGATTCGGTTGCTTCTAAAGCTCCATGTCCTGGGCT 1501
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QY 1502 AAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGATAAAC 1561
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QY 1562 AGAACATTTCTATGTACTACAACTGGTTTTTAAAAAGGAAGTATGTTGCTATGAAATAA 1621
Db 1784 AGAACATTTCTATGTACTACAACTGGTTTTTAAAAAGGAAGTATGTTGCTATGAAATAA 1843
QY 1622 ACTTGTGTCGTGTATAGGACAGCTGGATTTTTCATATTTCTTATTAATAATTTCTGCC 1681
Db 1844 ACTTGTGTCGTGTATAGGACAGCTGGATTTTTCATATTTCTTATTAATAATTTCTGCC 1903
QY 1682 ATTTAGAAGAGAGAACTACATTCATGTTTGAAGAGATAAACTCTGAAAGAGAGTGG 1741
Db 1904 ATTTAGAAGAGAGAACTACATTCATGTTTGAAGAGATAAACTCTGAAAGAGAGTGG 1963
QY 1742 CCTTATCTTCACCTTTATCGATAAGTCAGTTTATTTGTTTCATTTGTGTGTACATTTTATTT 1801
Db 1964 CCTTATCTTCACCTTTATCGATAAGTCAGTTTATTTGTTTCATTTGTGTGTACATTTTATTT 2023
QY 1802 CTCCTTTTGACATTAATACTGTTGGCTTTTCTAAATCTTGTAAATATATCTATTTTACC 1861
Db 2024 CTCCTTTTGACATTAATACTGTTGGCTTTTCTAAATCTTGTAAATATATCTATTTTACC 2083
QY 1862 AAAGGTATTTAATTTCTTTTATGACAACTTAGATCAACTATTTTACCTTTGGTAAAT 1921
Db 2084 AAAGGTATTTAATTTCTTTTATGACAACTTAGATCAACTATTTTACCTTTGGTAAAT 2143
QY 1922 TTTTCTAAACACAAATTTATAGCCAGAGGAAACAAAGATGATATAAAATATTTGTGCC 1981
Db 2144 TTTTCTAAACACAAATTTATAGCCAGAGGAAACAAAGATG--ATATAAATATTTGTTC 2200
QY 1982 CTGGACAAAATACATGTATNTCCATCCCGGAATGTTGCTAGAGTTGGATTAACACCTGCA 2041
Db 2201 TCTGACAAAATACATGTATTT--CATCTCGTATGTTGCTAGAGTTAGATT--AATCTGCA 2258
QY 2042 TTTTAAAAAACCTGAAATGGGAANGAANTGTAAGTTGGCCAAANCCTTTTTTGAAAA 2101
Db 2259 TTTTAAAAAACCTGAAAT--GGAATAGAATTTGTAAGTT--GCAAAAGACTTTTTTGAAAA 2312
QY 2102 TAATTAA 2108
Db 2313 TAATTAA 2319

RESULT 3

ABS57294

ID ABS57294 standard; DNA; 2825 BP.

XX ABS57294;

AC ABS57294;

XX ABS57294;

DT 31-JAN-2003 (first entry)

XX DNA encoding human vascular endothelial cell growth factor-E (VEGF-E).

DE Human; vascular endothelial cell growth factor-E; VEGF-E; PRO:200;

XX VEGF; bone morphogenetic protein 1; wound repair; tissue regeneration;

KW cardiovascular disorder; endothelial disorder; angiogenic disorder;

KW cancer; diabetes mellitus; cardiac hypertrophy; atherosclerosis;

KW cardiant; cytostatic; antidiabetic; antiarteriosclerotic;

KW gene therapy; gene; ds.

XX Homo sapiens.

OS Homo sapiens.

XX Key

FH Location/Qualifiers

FT 259..1296

FT /*tag= a

FT /product= "VEGF-E"

Db 1784 AGAACATCTATGCTACTCAAACTGGTTTAAAAAGGAAGTATGTTGCTATGAATTA 1843
Qy 1622 ACTTGTGTCGTGATAGACAGCTGGATTTTTCATATTTCTTAAATTTCTGCC 1681
Db 1844 ACTTGTGTCGTGATAGACAGCTGGATTTTTCATATTTCTTAAATTTCTGCC 1903
Qy 1682 ATTAGAAGAAGAACTACATTCATGGTTGGAAGAGATAAACCTGAAAGAGAGTGG 1741
Db 1904 ATTAGAAGAAGAACTACATTCATGGTTGGAAGAGATAAACCTGAAAGAGAGTGG 1963
Qy 1742 CCTATCTTCACCTTATCGATAAGTCAGTTTATTTGTTTCATTTGTGTACATTTTATAT 1801
Db 1964 CCTATCTTCACCTTATCGATAAGTCAGTTTATTTGTTTCATTTGTGTACATTTTATAT 2023
Qy 1802 CTCCTTTTGACATTAACCTGTTGGCTTTTCTAATCTTGTAAATATATCTATTTTACC 1861
Db 2024 CTCCTTTTGACATTAACCTGTTGGCTTTTCTAATCTTGTAAATATATCTATTTTACC 2083
Qy 1862 AAGGTATTAAATATCTTTTATGCAACTTAGATCAACTATTTTAGCTTGGTAAAT 1921
Db 2084 AAGGTATTAAATATCTTTTATGCAACTTAGATCAACTATTTTAGCTTGGTAAAT 2143
Qy 1922 TTTTCTAAACAAATTTGTTATAGCCAGAGCAAGATGGATATAAAATATTTGTC 1981
Db 2144 TTTTCTAAACAAATTTGTTATAGCCAGAGCAAGATGGATATAAAATATTTGTC 2200
Qy 1982 CTGCAAAAATACATGTTATNTCCATCCCGAATGGTGTAGAGTTGGATTAACTGCA 2041
Db 2201 TCTGCAAAAATACATGTTATNTCCATCCCGAATGGTGTAGAGTTGGATTAACTGCA 2258
Qy 2042 TTTTAAAAACCTGAATTTGGGAANGAANTGGTAAGTTGGCCAAANCTTTTTTGA 2101
Db 2259 TTTTAAAAACCTGAATTTGGGAANGAANTGGTAAGTTGGCCAAANCTTTTTTGA 2312
Qy 2102 TAATTA 2108
Db 2313 TAATTA 2319

RESULT 4
AAA47452
ID AAA47452 standard; cDNA; 2839 BP.
XX AAA47452;
AC AAA47452;
XX
DT 20-OCT-2000 (first entry)
XX
DE Human TANGO 128 coding sequence.
XX
KW TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma;
KW graft versus-host diseases; rheumatoid arthritis; psoriasis;
KW inflammatory bowel disease; septic shock; ulcerative colitis;
KW Crohn's disease; chronic myelogenous leukemia; cancer; liver
KW disease; Hodgkin's disease; osteoarthritis; Lyme's disease;
KW cachexia; autoimmune disease; myasthenia gravis; autoimmune diabetes;
KW systemic lupus erythematosus; transgenic animal; diagnosis;
KW prognosis; prophylactic; therapeutic; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 288..1325
FT /*tag= a
FT /product= TANGO 128
XX
PN WO200039284-A1.
XX
PD 06-JUL-2000.
XX
PF 23-DEC-1999; 99WO-US31025.
XX
PR 30-DEC-1999; 98US-0223546.

XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Holtzman DA;
XX
DR WPI; 2000-465743/40.
XX P-PSDB; AAB01419.
XX
PT Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213,
PT 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid
PT arthritis, psoriasis and autoimmune diseases
XX
PS Claim 1; Fig 1; 209pp; English.
XX
CC Nucleic acids encoding TANGO polypeptides are useful as modulating
CC agents for regulating cellular processes like asthma, graft
CC versus-host diseases, rheumatoid arthritis, psoriasis, inflammatory
CC bowel disease, septic shock, ulcerative colitis, Crohn's disease,
CC chronic myelogenous leukemia, cancer, liver disease, Hodgkin's
CC disease, osteoarthritis, Lyme's disease, cachexia and autoimmune
CC diseases e.g. myasthenia gravis, autoimmune diabetes and systemic
CC lupus erythematosus. The nucleic acids are also useful for producing
CC transgenic animals and the TANGO polypeptides themselves. Partial
CC TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in
CC forensic biology, for diagnostic assays, prognostic assays,
CC pharmacogenomics and for monitoring clinical trials. TANGO
CC polypeptides are suitable for both prophylactic and therapeutic
CC methods for treating a subject at risk of a disorder or having a
CC disorder associated with aberrant TANGO expression. A wide range
CC of cellular disorders can be treated.
XX
SQ Sequence 2839 BP; 858 A; 532 C; 600 G; 849 T; 0 other;
Query Match 93.9%; Score 1979.4; DB 21; Length 2839;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;
QY 2 CCCGCGTGAGTGAGCTCTCACCCAGTCAGCCAAATAGAGCTCTTCGGGCTTCTCCTGG 61
Db 253 CCCGCGTGAGTGAGCTCTCACCCAGTCAGCCAAATAGAGCTCTTCGGGCTTCTCCTGC 312
QY 62 TGACATCTGCCCTGGCCGCCAGAGACGAGGAGCTCAGCGGGAATCCAACTGAGTAGTA 121
Db 313 TGACATCTGCCCTGGCCGCCAGAGACGAGGAGCTCAGCGGGAATCCAACTGAGTAGTA 372
QY 122 AATTCAGTTTTCAGACACAGGACAGAAAGAGTCAAGATCTCTCAGCATGAGAGAA 181
Db 373 AATTCAGTTTTCAGACACAGGAAACAGACGAGTCAAGATCTCTCAGCATGAGAGAA 432
QY 182 TTATTACTGTGTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCTCATCTATCCAA 241
Db 433 TTATTACTGTGTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCTCATCTATCCAA 492
QY 242 GAAATACGGTCTTGGTATGAGAGTTAGTAGCAGTAGAGGAAATATGATCGATCAACTTA 301
Db 493 GAAATACGGTCTTGGTATGAGAGTTAGTAGCAGTAGAGGAAATATGATCGATCAACTTA 552
QY 302 CGTTTGATGAAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTG 361
Db 553 CGTTTGATGAAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTG 612
QY 362 TAGAAGTTGAGGAACCCAGTGATGAACTATATTAGGGCGCTGGTGTGGTCTGGTACTG 421
Db 613 TAGAAGTTGAGGAACCCAGTGATGAACTATATTAGGGCGCTGGTGTGGTCTGGTACTG 672
QY 422 TACCAGGAAAACAGATTTCTAAAGAAATCAAATTTAGGATAGATTTGTATCTGATGAAT 481
Db 673 TACCAGGAAAACAGATTTCTAAAGAAATCAAATTTAGGATAGATTTGTATCTGATGAAT 732
QY 482 ATTTTCCTTCTGAACACAGGTTTCTGCATCCACTACAAATTGTGTATGCCAATTCACAG 541
Db 733 ATTTTCCTTCTGAACACAGGTTTCTGCATCCACTACAAATTGTGTATGCCAATTCACAG 792

542	QY	AAAGCTGTGAGTCTCTTCAGTGTCTAACCCCTTCAGCTTTGCCATCTGACACCTGCTTAATAATG	601
793	DB	AAAGCTGTGAGTCTCTTCAGTGTCTAACCCCTTCAGCTTTGCCATCTGACACCTGCTTAATAATG	852
602	QY	CTATAACTCGCTTTTAGTACTCTTGGAGACCTTATTCGATATCTTGAAACAGAGAGATGCG	661
853	DB	CTATAACTCGCTTTTAGTACTCTTGGAGACCTTATTCGATATCTTGAAACAGAGAGATGCG	912
662	QY	AGTTGGACTTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGCCAAAGCTTTTGTTT	721
913	DB	AGTTGGACTTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGCCAAAGCTTTTGTTT	972
722	QY	TTTGAAGAAAAATCCAGAGTGTGGATCTGAACTTCTTAACAGAGGAGGTAAAGATTATACA	781
973	DB	TTTGAAGAAAAATCCAGAGTGTGGATCTGAACTTCTTAACAGAGGAGGTAAAGATTATACA	1032
782	QY	GCTGCAACACTCGTAACTCTCTCAGTGTCCATAGGGAAGAACTTAAAGAGAACCGATACCA	841
1033	DB	GCTGCAACACTCGTAACTCTCTCAGTGTCCATAGGGAAGAACTTAAAGAGAACCGATACCA	1092
842	QY	TTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTGGTGGGAACCTGTGCTGTGTCTCTCC	901
1093	DB	TTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTGGTGGGAACCTGTGCTGTGTCTCTCC	1152
902	QY	ACAATTTGCAATGAATGTCAATGTGTCCAAAGCAAAAGTTACTTAAAAAATAACCAAGAGTCC	961
1153	DB	ACAATTTGCAATGAATGTCAATGTGTCCAAAGCAAAAGTTACTTAAAAAATAACCAAGAGTCC	1212
962	QY	TTCAAGTTGAGACAAGAACCGGTGTGACGGGATTTGCACAAATCACTCAACGAGTGGCCC	1021
1213	DB	TTCAAGTTGAGACAAGAACCGGTGTGACGGGATTTGCACAAATCACTCAACGAGTGGCCC	1272
1022	QY	TGCAGCACCATAGGAGTGTGACTGTGTGACAGAGGAGCACAGGAGGATACCCGCATC	1081
1273	DB	TGCAGCACCATAGGAGTGTGACTGTGTGACAGAGGAGCACAGGAGGATACCCGCATC	1332
1082	QY	ACCACGACGACTCTTTGCCCAGAGCTGTGCAGTGCAGTGTGCTGAATTTATTAGAGAACGTT	1141
1333	DB	ACCACGACGACTCTTTGCCCAGAGCTGTGCAGTGCAGTGTGCTGAATTTATTAGAGAACGTT	1392
1142	QY	ATCGGTTATCTCCATCCTTAAATCTCAGTTGTGTTTGCTTCAGGACCTTTCACTCTCAGGAT	1201
1393	DB	ATCGGTTATCTCCATCCTTAAATCTCAGTTGTGTTTGCTTCAGGACCTTTCACTCTCAGGAT	1452
1202	QY	TTACAGTGCATTTCTGAAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACAGCTCTT	1261
1453	DB	TTACAGTGCATTTCTGAAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACAGCTCTT	1512
1262	QY	TTGAGAGGAGGCTTAAAGGACAGGAGAAAGGTCCTCAATCGTGGAAAGAAATTAATG	1321
1513	DB	TTGAGAGGAGGCTTAAAGGACAGGAGAAAGGTCCTCAATCGTGGAAAGAAATTAATG	1572
1322	QY	TTGTATTAAATAGATCACCAAGCTAGTTTTCAGAGTTTACCATGTACGTTATCCACTAGCTGG	1381
1573	DB	TTGTATTAAATAGATCACCAAGCTAGTTTTCAGAGTTTACCATGTACGTTATCCACTAGCTGG	1632
1382	QY	GTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTGAGTACAGAAAAAAACTG	1441
1633	DB	GTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTGAGTACAGAAAAAAACTG	1692
1442	QY	TGCAAGTGTGACACTGATTCGGTTGCTTAACTCTAAAGCTCCATGTCTCTGGGCGCT	1501
1693	DB	TGCAAGTGTGACACTGATTCGGTTGCTTAACTCTAAAGCTCCATGTCTCTGGGCGCT	1752
1502	QY	AAAAATCGTATAAAAATCTGGATTTTTTTTTTTTTTTTTTTTTTTTTGCTCATATTCATAAACC	1561
1753	DB	AAAAATCGTATAAAAATCTGGATTTTTTTTTTTTTTTTTTTTTTTTTGCTCATATTCATAAACC	1812
1562	QY	AGAACATTCATGTACTACAAACCTGGTTTTTTTAAABAGGAACTATGTTGCTATGCAATTA	1621
1813	DB	AGAACATTCATGTACTACAAACCTGGTTTTTTTAAABAGGAACTATGTTGCTATGCAATTA	1872
1622	QY	ACTTGTGTCGTGTGATAGGACAGACTGGATTTTTTTTCAATTTCTTTATTAATAATTTCTGCC	1681

Db	1873	ACTTGTGTCGTGTAAGACAGACTGGATTTTTCATATTTCTTATTAATAATTTCTGCC	1932
Qy	1682	ATTTAGAAGAAGAACTACATTTCATGGTTTGAAGAGATAAAACCTCAAAGAAGAGTGG	1741
Db	1933	ATTTAGAAGAAGAACTACATTTCATGGTTTGAAGAGATAAAACCTCAAAGAAGAGTGG	1992
Qy	1742	CCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTTGTCGTACATTTTATATT	1801
Db	1993	CCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTTGTCGTACATTTTATATT	2052
Qy	1802	CTCCTTTTGACATTAATAACTTGTTGGCTTTTCTAAATCTTGTAAATATATCTATTTTACC	1861
Db	2053	CTCCTTTTGACATTAATAACTTGTTGGCTTTTCTAAATCTTGTAAATATATCTATTTTACC	2112
Qy	1862	AAAGGATTTTAAATATCTTTTATGACAACTTAGATCAACTATTTTACGTTGGTAAAT	1921
Db	2113	AAAGGATTTTAAATATCTTTTATGACAACTTAGATCAACTATTTTACGTTGGTAAAT	2172
Qy	1922	TTTCTTAAACACAAATGTTTATAGCCGAGAGAACAAAGATGGATATAAAAATATTTGTGCC	1981
Db	2173	TTTCTTAAACACAAATGTTTATAGCCGAGAGAACAAAGATGGATATAAAAATATTTGTGCC	2229
Qy	1982	CTGCACAAAATACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAACCTGCA	2041
Db	2230	CTGCACAAAATACATGTATTTT-CATTCTCGTATGGTGCTAGAGTTAGATT-AACTGCA	2287
Qy	2042	TTTCTTAAACACCTGAATTTGGGAANGGAANTTGGTAAGGTTGGCCAAANCCTTTTGGAAA	2101
Db	2288	TTTCTTAAACACCTGAATTT--GGAAATAGATTGGTAAGTT--GCAAGACCTTTTGGAAA	2341
Qy	2102	TAATTAA 2108	
Db	2342	TAATTAA 2348	
RESULT 5			
AAZ34296			
ID AAZ34296 standard; cDNA; 2849 BP.			
XX	AC	AAZ34296;	
XX	DT	07-DEC-1999 (first entry)	
XX	DE	Human PRO200 nucleotide sequence.	
XX	KW	Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;	
XX	KW	probe; blood coagulation disorder; cancer; cellular adhesion disorder;	
XX	KW	secreted protein; transmembrane protein; ss.	
OS	OS	Homo sapiens.	
XX	FN	W09946281-A2.	
XX	PD	16-SEP-1999.	
XX	FF	08-MAR-1999; 99WO-US05028.	
XX	FR	10-MAR-1998; 98US-0077450.	
XX	FR	11-MAR-1998; 98US-0077632.	
XX	FR	11-MAR-1998; 98US-0077641.	
XX	FR	11-MAR-1998; 98US-0077649.	
XX	FR	12-MAR-1998; 98US-0077791.	
XX	FR	13-MAR-1998; 98US-0078004.	
XX	FR	17-MAR-1998; 98US-0040220.	
XX	FR	20-MAR-1998; 98US-0078886.	
XX	FR	20-MAR-1998; 98US-0078910.	
XX	FR	20-MAR-1998; 98US-0078936.	
XX	FR	20-MAR-1998; 98US-0078939.	
XX	FR	25-MAR-1998; 98US-0079294.	
XX	FR	26-MAR-1998; 98US-0079656.	
XX	FR	27-MAR-1998; 98US-0079663.	
XX	FR	27-MAR-1998; 98US-0079664.	

850 CTATAAAGTGGCTTTAGTACCTTGAAGACCTTATTCGATATCTTTGAACCCAGAGAGATGGC 909
 909
 662 AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGCTTTTGTGTT 721
 721
 910 AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGCTTTTGTGTT 969
 969
 722 TTGGAAGAAATCCAGAGTGTGATCTGAACCTTCTAAACAGAGAGGTAAAGATTATACA 781
 781
 970 TTGGAAGAAATCCAGAGTGTGATCTGAACCTTCTAAACAGAGAGGTAAAGATTATACA 1029
 1029
 782 GCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCA 841
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 1030 GCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCA 1089
 1089
 842 TTTTCTGCGCAGGTGTCTCTGTTTAAACGCTGTGTGGGAACTGTGCTGTGCTCTCC 901
 901
 1090 TTTTCTGCGCAGGTGTCTCTGTTTAAACGCTGTGTGGGAACTGTGCTGTGCTCTCC 1149
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 902 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTACTTAAATAATACCAGAGTCC 961
 961
 1150 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTACTTAAATAATACCAGAGTCC 1209
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 962 TTCAGTTGAGACCAAGACCGGTGTCAAGGGAATGCACAAATCACTCAACGAGTGGCCC 1021
 1021
 1210 TTCAGTTGAGACCAAGACCGGTGTCAAGGGAATGCACAAATCACTCAACGAGTGGCCC 1269
 1269
 1022 TGGACACCATGAGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGGTAGCCGATC 1081
 1081
 1270 TGGACACCATGAGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGGTAGCCGATC 1329
 1329
 1082 ACCACGACGCTCTTGGCCAGAGCTGTGCAAGTGTGAGTGTGCAACAGTCTT 1141
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 1330 ACCACGACGCTCTTGGCCAGAGCTGTGCAAGTGTGAGTGTGCAACAGTCTT 1389
 1389
 1142 ATGGTTATCTCCATCTTAATCTCAGTGTGTGCTTCAAGGACCTTTCATCTTCAGAT 1201
 1201
 1390 ATGGTTATCTCCATCTTAATCTCAGTGTGTGCTTCAAGGACCTTTCATCTTCAGAT 1449
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 1202 TTACAGTGCATCTTGAAGAGGAGACATCAACAGAAATTAGGAGTGTGCAACAGTCTT 1261
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 1450 TTACAGTGCATCTTGAAGAGGAGACATCAACAGAAATTAGGAGTGTGCAACAGTCTT 1509
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 1262 TTGAGAGAGGCTTAAAGGACAGGAGAAAGGTCTCAATCGTGGAAAGAAATTAATG 1321
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 1510 TTGAGAGAGGCTTAAAGGACAGGAGAAAGGTCTCAATCGTGGAAAGAAATTAATG 1569
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 1322 TTGATTAATAATAGATCACAGCTAGTTTTCAGAGTTTACCATGTACGTATTCACATAGCTGG 1381
 1381
 1570 TTGATTAATAATAGATCACAGCTAGTTTTCAGAGTTTACCATGTACGTATTCACATAGCTGG 1629
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 1382 GTTCTGTATTCAGTCTTTCGATACCGCTTAGGGTAATGTACAGTACAGGAAAAAATCTG 1441
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 1630 GTTCTGTATTCAGTCTTTCGATACCGCTTAGGGTAATGTACAGTACAGGAAAAAATCTG 1689
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 1442 TGCAAGTACAGACCTGATTCGTTGCTTCAATCTTAAGCTTCAATGTCCTGGGCT 1501
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 1690 TGCAAGTACAGACCTGATTCGTTGCTTCAATCTTAAGCTTCAATGTCCTGGGCT 1749
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 1750 AAAATCGTATAAAATCTCGAATTTTTTTTTTTTTTTTCTCATATTCATATGTAAC 1809
 1809
 1562 AGAATCTGTACTACTACAACTGGTATTTTAAAGGAACTATGTTCTATGAATTA 1621
 1621
 1810 AGAATCTGTACTACTACAACTGGTATTTTAAAGGAACTATGTTCTATGAATTA 1869
 1869
 1622 ACTTGTGCTCTCATAGGACAGACTGGATTTTTTCAATTTCTTATTAATTAATTTCTGCC 1681
 1681
 1870 ACTTGTGCTCTCATAGGACAGACTGGATTTTTTCAATTTCTTATTAATTAATTTCTGCC 1929
 1929
 1682 ATTTAGAGAGAGAACTACATTCATGTTTGGAAAGATTAACCTGAAAGAGAGTGG 1741
 1741

1930 ATTTAGAGAGAGAACTACATTCATGTTTGGAGAGATAACTGAAAGAGAGTGG 1989
 1989
 1742 CTTTATCTTCACTTATCGATTAAGTCACTTATTTGTTTTCATTTGTTGATCAATTTTATAT 1801
 1801
 1990 CTTTATCTTCACTTATCGATTAAGTCACTTATTTGTTTTCATTTGTTGATCAATTTTATAT 2049
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 1802 CTCCCTTTGACATTAATCACTGTTGGCTTTTCTAACTTGTGTTAAATATATCTATTTTACC 1861
 1861
 2050 CTCCCTTTGACATTAATCACTGTTGGCTTTTCTAACTTGTGTTAAATATATCTATTTTACC 2109
 2109
 1862 AAAGGTATTTAATATTTCTTTTATGACAACTTAGATCAACTATTTTAGCTTGGTAAT 1921
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 2110 AAAGGTATTTAATATTTCTTTTATGACAACTTAGATCAACTATTTTAGCTTGGTAAT 2169
 2169
 1922 TTTTCTAAACACAAATTTATAGCCAGAGGACAAAGATGATATAAATAATATTTGTC 1981
 1981
 2170 TTTTCTAAACACAAATTTATAGCCAGAGGACAAAGATGATATAAATAATATTTGTC 2226
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 1982 CTGGACAAAAATACATGTATNTCCATCCCGAATGCTGCTAGAGTTGGATTAACCTGCA 2041
 2041
 2227 TCTGACAAAAATACATGTATTT-CATTCCTGATGCTGCTAGAGTTAGATT-AACTGCA 2284
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 2042 TTTTAAAAAACCCTGAATTTGGGAANGAANTTGGTAAGTTGGCCAAANCTTTTGTGAAA 2101
 2101
 2285 TTTTAAAAAACCCTGAATTT---GGAATAGATTTGGTAAGTT---GCAAGAGACTTTTGTGAAA 2338
 2338
 2102 TAATTA 2108
 2339 TAATTA 2345

RESULT 6

AAC78582

ID AAC78582 standard; cdNA; 2849 BP.

AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

XX AC AAC78582;

Human PRO200 (UNQ174) nucleotide sequence SEQ ID NO:487.

Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
expressed sequence tag; detection; cancer; ss.

Homo sapiens.

WO200053756-A2.

14-SEP-2000.

18-FEB-2000; 2000WO-US04341.

08-MAR-1999; 99WO-US05028.

12-MAR-1999; 99US-0123957.

29-MAR-1999; 99US-0126773.

21-APR-1999; 99US-0130232.

28-APR-1999; 99US-0131445.

14-MAY-1999; 99US-0134287.

23-JUN-1999; 99US-0141037.

26-JUL-1999; 99US-0145698.

29-OCT-1999; 99US-0162506.

30-NOV-1999; 99WO-US28313.

02-DEC-1999; 99WO-US28551.

02-DEC-1999; 99WO-US28565.

16-DEC-1999; 99WO-US30095.

30-DEC-1999; 99WO-US31243.

30-DEC-1999; 99WO-US31274.

05-JAN-2000; 2000WO-US00219.

06-JAN-2000; 2000WO-US00277.

06-JAN-2000; 2000WO-US00376.

(GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MB, PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI; XX WPI; 2000-611443/58.

DR P-PSDB; AAB44322.

XX Novel PRO polypeptides and polynucleotides used in detection methods, PT to target bioactive molecules to specific cells, and to modulate PT cellular activities -

XX Claim 2; Fig 206; 636pp; English.

XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic CC activity. The polynucleotides and polypeptides can be used for detecting CC the presence of PRO polypeptides in samples, for linking bioactive CC molecules to cells and for modulating biological activities of cells, CC using the polypeptides for specific targeting. The polypeptide targeting CC can be used to kill the target cells, e.g. for the treatment of cancers. CC The polypeptide pairs provide specific targeting of bioactive molecules CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in CC the isolation of the PRO polynucleotide sequences.

XX Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Query Match 93.9%; Score 1979.4; DB 21; Length 2849;
Best Local Similarity 97.7%; Pred. NO. 0;
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

QY 2 CCCGCGGTGAGTACCTCTACCCCGAGTCAGCAAAAGAGCTCTTCGGGCTTCCTCGG 61
DB 250 CCCGCGGTGAGTACCTCTACCCCGAGTCAGCAAAAGAGCTCTTCGGGCTTCCTCGG 309
QY 62 TGACATCTGCCCTGCGCGGCAGAGACGAGGAGCTCAGCGGAACTCAACCTGAGTAGTA 121
DB 310 TGACATCTGCCCTGCGCGGCAGAGACGAGGAGCTCAGCGGAACTCAACCTGAGTAGTA 369
QY 122 AATTCAGTTTCCAGCAACGAGGACAGAGCGGAGTACAGATCCTCAGCATGAGAGAA 181
DB 370 AATTCAGTTTCCAGCAACGAGGACAGAGCGGAGTACAGATCCTCAGCATGAGAGAA 429
QY 182 TTATTACTGTCTACTAATGGAAGTATTCACGCCCAAGGTTTCTCATACTTATCCAA 241
DB 430 TTATTACTGTCTACTAATGGAAGTATTCACGCCCAAGGTTTCTCATACTTATCCAA 489
QY 242 GAATACCGTCTTGTGATGGAGNTAGTACAGTAGAGGAAATGTATGATACAACTTA 301
DB 490 GAATACCGTCTTGTGATGGAGNTAGTACAGTAGAGGAAATGTATGATACAACTTA 549
QY 302 CGTTTGATGAAGATTTTGGGCTTGAAGACCCAGAGATGAATATGCAAGTATGATTTTG 361
DB 550 CGTTTGATGAAGATTTTGGGCTTGAAGACCCAGAGATGAATATGCAAGTATGATTTTG 609
QY 362 TAGAAGTTGAGAACCCAGTATGAACTATATTAGGCGCTGTTGGTTCGTGACTG 421
DB 610 TAGAAGTTGAGAACCCAGTATGAACTATATTAGGCGCTGTTGGTTCGTGACTG 669
QY 422 TACAGGAAACACAGATTTCTAAAGGAAATCAATATTAGGATGAAGTATGATCTGATCAAT 481
DB 670 TACAGGAAACACAGATTTCTAAAGGAAATCAATATTAGGATGAAGTATGATCTGATCAAT 729
QY 482 ATTTTCCTTGAACACAGGTTTCTGATCCACTCAACATTTGTCATGCCAATTCACAG 541
DB 730 ATTTTCCTTGAACACAGGTTTCTGATCCACTCAACATTTGTCATGCCAATTCACAG 789
QY 542 AAGCTGTGAGTCTTCACTGCTACCCCTTCCAGCTTTTCCAGCTGCTGCTTAATG 601
DB 790 AAGCTGTGAGTCTTCACTGCTACCCCTTCCAGCTTTTCCAGCTGCTGCTTAATG 849

QY 602 CTATTAACCTGCTTTAGTACCTTGGAGAGACCTTATTTCGATATCTTGAACACAGAGATGCG 661
DB 850 CTATTAACCTGCTTTAGTACCTTGGAGAGACCTTATTTCGATATCTTGAACACAGAGATGCG 909
QY 662 AGTTGGACCTTAGAAGATCTATATAGCCCAACTTGGCAACTCTTCTGGCAAGGCTTTTGT 721
DB 910 AGTTGGACCTTAGAAGATCTATATAGCCCAACTTGGCAACTCTTCTGGCAAGGCTTTTGT 969
QY 722 TTGGAGAAATCCAGAGTGGTGAATCTGAACCTTCTAACAGAGAGGTAGATTAACA 781
DB 970 TTGGAGAAATCCAGAGTGGTGAATCTGAACCTTCTAACAGAGAGGTAGATTAACA 1029
QY 782 GCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGAGAGAACTAAAGAGAACCGATACA 841
DB 1030 GCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGAGAGAACTAAAGAGAACCGATACA 1089
QY 842 TTTTCTGGCCAGGTTGTCTCTCGTTTAAACCGCTGTGGTGGAACTGTGCCTGTCTCTCC 901
DB 1090 TTTTCTGGCCAGGTTGTCTCTCGTTTAAACCGCTGTGGTGGAACTGTGCCTGTCTCTCC 1149
QY 902 ACATTTGCAATGAATGTCAATGTCTCCAGAGCAAAAGTTACTTAAATAATACACAGAGTCC 961
DB 1150 ACAATTTGCAATGAATGTCAATGTCTCCAGAGCAAAAGTTACTTAAATAATACACAGAGTCC 1209
QY 962 TTCAGTTGAGACCAAGACCGGTGTCCAGGAGTTCACAAATCACTCACCCAGCTGGCCC 1021
DB 1210 TTCAGTTGAGACCAAGACCGGTGTCCAGGAGTTCACAAATCACTCACCCAGCTGGCCC 1269
QY 1022 TGGAGCACCATGAGAGTGTGACTGTGTGTGAGAGGAGGACACAGAGGATAGCCGATC 1081
DB 1270 TGGAGCACCATGAGAGTGTGACTGTGTGTGAGAGGAGGACACAGAGGATAGCCGATC 1329
QY 1082 ACCACAGCAGCTCTTGGCCAGAGCTGTCCAGTGTGAGTGGCTGATTTATTAGAGAACT 1141
DB 1330 ACCACAGCAGCTCTTGGCCAGAGCTGTCCAGTGTGAGTGGCTGATTTATTAGAGAACT 1389
QY 1142 ATGCGTTATCTCACTCTTAAATCTCAGTTTGTGTTTCAAGACCTTTCATCTTCAGGAT 1201
DB 1390 ATGCGTTATCTCACTCTTAAATCTCAGTTTGTGTTTCAAGACCTTTCATCTTCAGGAT 1449
QY 1202 TTACAGTGTATCTGAGAGGAGGACATCAACAGAAATAGAGTTGTGCAACAGCTCTT 1261
DB 1450 TTACAGTGTATCTGAGAGGAGGACATCAACAGAAATAGAGTTGTGCAACAGCTCTT 1509
QY 1262 TTGAGAGGAGGCTTAAAGGACAGGAGAAAGGTCTTCAATCGTGGAAAGAAATTTAAATG 1321
DB 1510 TTGAGAGGAGGCTTAAAGGACAGGAGAAAGGTCTTCAATCGTGGAAAGAAATTTAAATG 1569
QY 1322 TTGTATTAATAGATCACCGCTAGTTTCAGAGTTTACCATGTACCTATTCCTAGCTGG 1381
DB 1570 TTGTATTAATAGATCACCGCTAGTTTCAGAGTTTACCATGTACCTATTCCTAGCTGG 1629
QY 1382 GTTCTGTATTTCAGTCTTTTCGATACGCTTAAAGTAAATGTCTAGTACAGAGAAACCTG 1441
DB 1630 GTTCTGTATTTCAGTCTTTTCGATACGCTTAAAGTAAATGTCTAGTACAGAGAAACCTG 1689
QY 1442 TGCAGTGTAGACCTGATTCGCTTGCCTTAACTTAAAGCTTCCATGTCTGGGCT 1501
DB 1690 TGCAGTGTAGACCTGATTCGCTTGCCTTAACTTAAAGCTTCCATGTCTGGGCT 1749
QY 1502 AAAATCGTATAAATCTGGATTTTCTGCTCATATTTCTCATATTTGATTAAC 1561
DB 1750 AAAATCGTATAAATCTGGATTTTCTGCTCATATTTCTCATATTTGATTAAC 1809
QY 1562 AGAATCTTATGTACTACAAACCTGGTTTAAAGAGAACTATGTCTATGATTA 1621
DB 1810 AGAATCTTATGTACTACAAACCTGGTTTAAAGAGAACTATGTCTATGATTA 1869
QY 1622 ACTGTGTCTCTGATGAGACAGACTGGATTTTCTATTTCTTATTAATTTCTGCC 1681
DB 1870 ACTGTGTCTCTGATGAGACAGACTGGATTTTCTATTTCTTATTAATTTCTGCC 1929
QY 1682 ATTTAGAGAGAGAACTACATTTCTGTTTGGAGAGATAAACCTGAAAGAGAGTGG 1741

1930 ATTTAGAGAGAGAACTCAATTCATGGTTTGAAGAGATAAACCCTGAAAGAGAGTGG 1989
 1742 CCTTATCTTCACATTTATCGATAGTCAAGTTATTTGTTTCATTTGTTACATTTTATATT 1801
 1990 CCTTATCTTCACATTTATCGATAGTCAAGTTATTTGTTTCATTTGTTACATTTTATATT 2049
 1802 CTCCTTTTGACATATAACCTGGTGGCTTTCTTAATCTTGTAAATATATCTATTTTACC 1861
 2050 CTCCTTTTGACATATAACCTGGTGGCTTTCTTAATCTTGTAAATATATCTATTTTACC 2109
 1862 AAGAGTATTATTAATCTTTTATGACAACTTAGATCAACTATTTTATAGCTTGGTAAAT 1921
 2110 AAGAGTATTATTAATCTTTTATGACAACTTAGATCAACTATTTTATAGCTTGGTAAAT 2169
 1922 TTTTCTAAACAAATTTGTTATAGCCAGAGAAACAAAGATGATATAAAATATTTGTCG 1981
 2170 TTTTCTAAACAAATTTGTTATAGCCAGAGAAACAAAGATG---ATATAAATATTTGTCG 2226
 1982 CTGACAAAATACATGTAATNTCCATCCCGAATGGTCTAGAGTTGGATTAAACCTGCA 2041
 2227 TCTGACAAAATACATGTAATNT---CATCTCGTATGGTCTAGAGTTAGATT---AATCTGCA 2284
 2042 TTTTAAACAACTCAATTTGGGAANGGAANTTTGTAAGTTGGCCAAANCTTTTTCGAAA 2101
 2285 TTTTAAACAACTCAATTT---GGAATAGAAATTTGGTAAGTT---GCAAAAGACTTTTTCGAAA 2338
 2102 TAATTTA 2108
 2339 TAATTTA 2345

RESULT 7

AAA88515

ID AAA88515 standard; cDNA; 2849 BP.

XX AAA88515;

AC 22-JAN-2001 (first entry)

DE Human PRO200 (VEGF-E) cDNA clone DNA29101-1272.

XX PRO200; vascular epithelial growth factor E; VEGF-E; human;
 KW ocular disease; retinopathy; maculopathy; therapy;
 KW retinitis pigmentosa; macular degeneration; retinal detachment;
 KW retinal tear; macular hole; myopia; traumatic chorioretinopathy;
 KW acute retinal necrosis syndrome; contusion; edema;
 KW retinal vision occlusion; vascular disease; retinal vasculitis;
 KW thrombocytopenic purpura; uveitis; retinal occlusion; ss.

XX Homo sapiens.

Key	Location/Qualifiers
PH CDS	285..1322
FT	/*tag= a
FT	sig_peptide 285..326
FT	/*tag= b
FT	mat_peptide 327..1319
FT	/*tag= c

XX WO200053760-A2.

XX 14-SEP-2000.

XX 10-MAR-2000; 2000WO-US06319.

XX 12-MAR-1999; 99US-0123957.

XX (GETH) GENENTECH INC.

XX Ferrara N, Goddard A, Gurney AL, Hebert C, Henzel WJ, Kabakoff RC;
 PI Klein RD, Kijavini IJ, Kuo SS, La Fleur M, Wood WI;

XX

DR WPI: 2000-587437/55.
 DR P-PSDB; AAB19578.

XX Novel PRO polypeptides useful for preventing or rescuing retinal cells
 PT from injury caused by ocular diseases such as retinitis pigmentosa,
 PT retinopathy, retinal degenerative diseases, degenerative myopia,
 PT uveitis -

XX Example 8; Fig 1; 140pp; English.

CC The present sequence is that of cDNA clone DNA29101-1272 or UNQ174
 CC (ATCC 20953) isolated from a human glioma cell line G61 cDNA
 CC library using probes (see AAA88523-26) based on an expressed sequence
 CC tag (see AAA88522) identified on the basis of homology to vascular
 CC endothelial growth factor (VEGF). The clone contains a single open
 CC reading frame encoding a 345-amino acid protein (see AAB19578)
 CC designated PRO200 or VEGF-E. The isolated cDNA can be used in the
 CC recombinant production of PRO200 (VEGF-E). The invention relates
 CC to the use of PRO polypeptides, including PRO200, to delay, prevent
 CC or rescue retinal cells such as retinal neurons selected from
 CC photoreceptors, retinal ganglion cells, displaced retinal ganglion
 CC cells, amacrine cells, displaced amacrine cells, horizontal and
 CC bipolar neurons, and supportive cells (including Mueller cells and
 CC pigment epithelial cells) from injury and degradation. The retinal
 CC cells are preferably photoreceptors and photoreceptor cell injury or
 CC death is caused by retinal injury, light or environmental trauma or
 CC by an ocular disease selected from retinitis pigmentosa, macular
 CC degeneration, including age-related, retinal detachment, retinal
 CC tears, retinopathy, retinal degenerative diseases, macular holes,
 CC degenerative myopia, acute retinal necrosis syndrome, traumatic
 CC chorioretinopathies or contusion such as Purtscher's retinopathy,
 CC edema, ischemic conditions such as central or branch retinal vision
 CC occlusion, collagen vascular diseases, thrombocytopenic purpura,
 CC uveitis, retinal vasculitis and occlusion associated with Eales
 CC disease and systemic lupus erythematosus (claimed).

XX Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Query Match 93.9%; Score 1979.4; DB 21; Length 2849;
 Best Local Similarity 97.7%; Pred. No. 0;
 Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

QY	2	CCGCCGCTGAGTGAGCTCTCACCCAGTCAGCAAAATGAGCTCTTCGGGCTTCTCTGGG	61
DB	250	CCGCCGCTGAGTGAGCTCTCACCCAGTCAGCAAAATGAGCTCTTCGGGCTTCTCTGGG	309
QY	62	TGACATCTGCCCTGCGCCGAGACGAGGAGCTCAGCGGAATCCCACTGAGTAGTA	121
DB	310	TGACATCTGCCCTGCGCCGAGACGAGGAGCTCAGCGGAATCCCACTGAGTAGTA	369
QY	122	AATTCAGTTTTCAGCAACAGGAACAGACGAGTCAAGATCCTCAGCATGAGAGAA	181
DB	370	AATTCAGTTTTCAGCAACAGGAACAGACGAGTCAAGATCCTCAGCATGAGAGAA	429
QY	182	TTATTACTGTGCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCTATCTATCCAA	241
DB	430	TTATTACTGTGCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCTATCTATCCAA	489
QY	242	GAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGAAAATGTATGATCAACTTA	301
DB	490	GAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGAAAATGTATGATCAACTTA	549
QY	302	CGTTTGATGAAGATTGGGCTTGAAGACCCGAGAGATGACATATGCAAGTATGATTTTG	361
DB	550	CGTTTGATGAAGATTGGGCTTGAAGACCCGAGAGATGACATATGCAAGTATGATTTTG	609
QY	362	TAGAAAGTTGAGGAACCCAGTATGAACTATATATTAGGCGCTGGTGTCTCTGCTACTG	421
DB	610	TAGAAAGTTGAGGAACCCAGTATGAACTATATATTAGGCGCTGGTGTCTCTGCTACTG	669
QY	422	TACCGAGAAAACAGATTTTCTAAAGGAAATCAAATTTAGGATAAGATTTTGTATCTGAT	481
DB	670	TACCGAGAAAACAGATTTTCTAAAGGAAATCAAATTTAGGATAAGATTTTGTATCTGAT	729

XX 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99US-0123618.
 PR 12-MAR-1999; 99US-0123957.
 PR 23-MAR-1999; 99US-0125775.
 PR 12-APR-1999; 99US-0128849.
 PR 20-APR-1999; 99WO-US08615.
 PR 28-APR-1999; 99US-0131445.
 PR 04-MAY-1999; 99US-0132371.
 PR 14-MAY-1999; 99US-0134287.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99WO-US02011.
 PR 01-SEP-1999; 99WO-US20594.
 PR 08-SEP-1999; 99WO-US20944.
 PR 13-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-OCT-1999; 99US-0162506.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30099.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PA (GETH) GENENTECH INC.
 XX AShtenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
 PI Stewart TA, Tumas G, Watanabe CK, Wood WI, Yan M;
 XX WPI: 2000-572271/53.
 DR P-PSDB; AAB33414.
 XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
 XX Claim 23; Fig 1; 309pp; English.
 XX The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
 CC autoimmune or immune-mediated skin diseases, allergic diseases,
 CC immunological diseases of the lung, and transplantation associated
 CC diseases including graft rejection and graft-versus-host-disease.
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and

CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;
 Query Match 93.9%; Score 1979.4; DB 21; Length 2849;
 Best Local Similarity 97.7%; Pred. No. 0;
 Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;
 QY 2 CCGCGCGTGAAGTCTCTCACCCCAGTCAGCCAAATAGAGCTCTTTCGGGCTTCCTCGG 61
 DB 250 CCGCGCGTGAAGTCTCTCACCCCAGTCAGCCAAATAGAGCTCTTTCGGGCTTCCTCGG 309
 QY 62 TGACATCTCGCTCGCGCCGAGAGCGGAGGACTCAGCGGAAATCCACCTGAGTAGTA 121
 DB 310 TGACATCTCGCTCGCGCCGAGAGCGGAGGACTCAGCGGAAATCCACCTGAGTAGTA 369
 QY 122 AATTCAGTTCCTCCAGCAACAAGGAGTACAGAGCGGAGTCAAGATCCTCAGCATGAGAGAA 181
 DB 370 AATTCAGTTCCTCCAGCAACAAGGAGTACAGAGCGGAGTCAAGATCCTCAGCATGAGAGAA 429
 QY 182 TTATTAAGTCTGCTACTAATGAAGTATTCACAGCCCAAGGTTTCTCTACTATTCCTCAA 241
 DB 430 TTATTAAGTCTGCTACTAATGAAGTATTCACAGCCCAAGGTTTCTCTACTATTCCTCAA 489
 QY 242 GAAATACGGTCTTGGTATGAGATAGTAGCAGTAGAGGAAATGTATGCATCAACTTAA 301
 DB 490 GAAATACGGTCTTGGTATGAGATAGTAGCAGTAGAGGAAATGTATGCATCAACTTAA 549
 QY 302 CGTTTGAAGAAGATTTGGGCTTGAAGCCGAGAGATGACATATGCAAGTAGTAGATTTTG 361
 DB 550 CGTTTGAAGAAGATTTGGGCTTGAAGCCGAGAGATGACATATGCAAGTAGTAGATTTTG 609
 QY 362 TAGAAGTTCAGGAACCCAGTGAAGAACTATATTAGGGCGCTGCTGCTCTGGTACTG 421
 DB 610 TAGAAGTTCAGGAACCCAGTGAAGAACTATATTAGGGCGCTGCTGCTCTGGTACTG 669
 QY 422 TACCAGGAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGATCGATGAAT 481
 DB 670 TACCAGGAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGATCGATGAAT 729
 QY 482 ATTTTCTCTTGAACCCAGGGTTCTGCATCCATCAGCAATTTGTCATGCCAATTCACAG 541
 DB 730 ATTTTCTCTTGAACCCAGGGTTCTGCATCCATCAGCAATTTGTCATGCCAATTCACAG 789
 QY 542 AAGCTGTGAGTCTCTCAGTGTCTACCCCTTTCAGCTTTGCACTTGGACCTGCTTAAATG 601
 DB 790 AAGCTGTGAGTCTCTCAGTGTCTACCCCTTTCAGCTTTGCACTTGGACCTGCTTAAATG 849
 QY 602 CTATACTGCTTTAGTACCTTGGAAAGACCTTATTGATATCTTGAACGAGAGATGGC 661
 DB 850 CTATACTGCTTTAGTACCTTGGAAAGACCTTATTGATATCTTGAACGAGAGATGGC 909
 QY 662 AGTTGGACTTTAGAAGATCTATATAGCCCAACTTGGCACTTCTTGGCAAGGCTTTTGT 721
 DB 910 AGTTGGACTTTAGAAGATCTATATAGCCCAACTTGGCACTTCTTGGCAAGGCTTTTGT 969
 QY 722 TTGGAAGAAATTCAGAGTGGTGGATCTGAACCTTCTAACAGAGAGGTAAGATTATACA 781
 DB 970 TTGGAAGAAATTCAGAGTGGTGGATCTGAACCTTCTAACAGAGAGGTAAGATTATACA 1029
 QY 782 GCTGCACACTCGTAACTCTCAGTGTCCATAGGAGGAACTAAGAGAACCGTATCCA 841
 DB 1030 GCTGCACACTCGTAACTCTCAGTGTCCATAGGAGGAACTAAGAGAACCGTATCCA 1089
 QY 842 TTTTCTGGCAGGTTGCTCTCCCTGGTTAAACGCTGTGGTGGGAACCTGCTGTCTCTCC 901
 DB 1090 TTTTCTGGCAGGTTGCTCTCCCTGGTTAAACGCTGTGGTGGGAACCTGCTGTCTCTCC 1149
 QY 902 ACAATTGCAATGAATGCTCAATGTGCTCCCAAGCAAGATTTACTAAAAATACCAAGAGTCC 961
 DB 1150 ACAATTGCAATGAATGCTCAATGTGCTCCCAAGCAAGATTTACTAAAAATACCAAGAGTCC 1209

CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
 CC cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors
 CC containing them and the PRO polypeptide may be used to treat disorders
 CC associated with decreased PRO expression. AAA77510 to AAA77721 and
 CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in
 CC the exemplification of the present invention.
 XX

SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Query Match 93.9%; Score 1979.4; DB 21; Length 2849;
 Best Local Similarity 97.7%; Pred. No. 0;
 Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

Qy	2	CCGCCGCTGAGTGGCTCTCACCCAGTCAGCCAAATGAGCCCTTCGGGCTTCCTCGG	61
Db	250	CCGCCGCTGAGTGGCTCTCACCCAGTCAGCCAAATGAGCCCTTCGGGCTTCCTCGG	309
Qy	62	TGACATCTGCCCTGGCCGCGCAGAGAGCGGAGTCCAGCGGAAATCCAACTGAGTAGTA	121
Db	310	TGACATCTGCCCTGGCCGCGCAGAGAGCGGAGTCCAGCGGAAATCCAACTGAGTAGTA	369
Qy	122	AATTCAGTTTCCAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCA	181
Db	370	AATTCAGTTTCCAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCA	429
Qy	182	TTATTAATCTGTCTACTAATGGAATATTCACAGCCCAAGGTTTCCTCTACTTATCCAA	241
Db	430	TTATTAATCTGTCTACTAATGGAATATTCACAGCCCAAGGTTTCCTCTACTTATCCAA	489
Qy	242	GAATACGGTCTGGTATGAGATTAGTAGCAGTAGGAGAAATGATGGATACAACTTA	301
Db	490	GAATACGGTCTGGTATGAGATTAGTAGCAGTAGGAGAAATGATGGATACAACTTA	549
Qy	302	CGTTTGATGAAGATTTGGGCTTGAGACCCAGAGATGACATATGCAAGTATGATTTTG	361
Db	550	CGTTTGATGAAGATTTGGGCTTGAGACCCAGAGATGACATATGCAAGTATGATTTTG	609
Qy	362	TAGAAATGAGGAACCCAGTGGTATATATAGGGCGCTGGTGGTCTGGTACTG	421
Db	610	TAGAAATGAGGAACCCAGTGGTATATATAGGGCGCTGGTGGTCTGGTACTG	669
Qy	422	TACAGGAATAACAGATTTCTAAAGGAATCAAAATAGGATAAGATTTGATCTGATGAAT	481
Db	670	TACAGGAATAACAGATTTCTAAAGGAATCAAAATAGGATAAGATTTGATCTGATGAAT	729
Qy	482	ATTTTCCTCTGAACCGAGGTTTGGATCCATCAACATGTGTCAGCCCAATTCACAG	541
Db	730	ATTTTCCTCTGAACCGAGGTTTGGATCCATCAACATGTGTCAGCCCAATTCACAG	789
Qy	542	AAGCTGTGAGTCTTCAGTGTCTACCCCTTCAGCTTTGCCACTGGACCTCTTAATAATG	601
Db	790	AAGCTGTGAGTCTTCAGTGTCTACCCCTTCAGCTTTGCCACTGGACCTCTTAATAATG	849
Qy	602	CTATACTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCCAGAGATGGC	661
Db	850	CTATACTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCCAGAGATGGC	909
Qy	662	AGTTGGACTTGAAGATCTATATAGGCAACTTGGCAACTTCTTGGCAAGGCTTTGTTT	721
Db	910	AGTTGGACTTGAAGATCTATATAGGCAACTTGGCAACTTCTTGGCAAGGCTTTGTTT	969
Qy	722	TTGGAAGAAATCCAGAGTGTGATCTGAACCTTCTAACAGAGAGGTAAATATACCA	781
Db	970	TTGGAAGAAATCCAGAGTGTGATCTGAACCTTCTAACAGAGAGGTAAATATACCA	1029
Qy	782	GCTGCACACCTCGTAATCTTCAGTGTCTCATAAGGAGAACTTAAGAGAACCGATACCA	841
Db	1030	GCTGCACACCTCGTAATCTTCAGTGTCTCATAAGGAGAACTTAAGAGAACCGATACCA	1089
Qy	842	TTTTCTGGCCAGGTTGCTCTCGTTAAACCGCTGTGGTGGAACTGTGCTGTGCTCC	901
Db	1090	TTTTCTGGCCAGGTTGCTCTCGTTAAACCGCTGTGGTGGAACTGTGCTGTGCTCC	1149

Qy	902	ACAAATTCBAATGATGTCATATGTCCTCCAGCAAGAGTTACTAAAAATACACAGAGTCC	961
Db	1150	ACAAATTCBAATGATGTCATATGTCCTCCAGCAAGAGTTACTAAAAATACACAGAGTCC	1209
Qy	962	TTCAATTTGAGACCAAAAGACCGGTGTGACGGGATTTGCAAAATCACTCACCGAGTGGCC	1021
Db	1210	TTCAATTTGAGACCAAAAGACCGGTGTGACGGGATTTGCAAAATCACTCACCGAGTGGCC	1269
Qy	1022	TGGAGCAACCATGAGGAGTGTGATGTCGTGTCAGAGGAGACAGAGGATACCCGATC	1081
Db	1270	TGGAGCAACCATGAGGAGTGTGATGTCGTGTCAGAGGAGACAGAGGATACCCGATC	1329
Qy	1082	ACCACCAAGCAGCTCTTCCGCCAGAGCTGTGCAAGTGCAGTGCCTGATTTCTATTAGAGAACGT	1141
Db	1330	ACCACCAAGCAGCTCTTCCGCCAGAGCTGTGCAAGTGCAGTGCCTGATTTCTATTAGAGAACGT	1389
Qy	1142	ATGGTTATCTCATCTTAAATCTCAGTGTGTTTCTCAAGGACCTTCACTTTCAGGAT	1201
Db	1390	ATGGTTATCTCATCTTAAATCTCAGTGTGTTTCTCAAGGACCTTCACTTTCAGGAT	1449
Qy	1202	TTACAGTGCATTTCTGAAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACAGCTCTT	1261
Db	1450	TTACAGTGCATTTCTGAAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACAGCTCTT	1509
Qy	1262	TTGAGAGAGGCGCTTAAAGGACAGAGAAAGGCTTCAATCGTGGAGAAAGAAATTAATG	1321
Db	1510	TTGAGAGAGGCGCTTAAAGGACAGAGAAAGGCTTCAATCGTGGAGAAAGAAATTAATG	1369
Qy	1322	TTGTATTAATAATAGATCAACAGTATGTTTCAAGTATACATGTACGTATTCACCTAGCTGG	1381
Db	1570	TTGTATTAATAATAGATCAACAGTATGTTTCAAGTATACATGTACGTATTCACCTAGCTGG	1629
Qy	1382	GTTCTGATTTTCACTTCTTTCGATACCGCTTAGGGTAAATGTCTAGTACAGGAAAAAACTG	1441
Db	1630	GTTCTGATTTTCACTTCTTTCGATACCGCTTAGGGTAAATGTCTAGTACAGGAAAAAACTG	1689
Qy	1442	TGCAAGTGTAGCAACCTGATTCGGTTGCTTCAACCTTAAAGCTTCAAGTCTTGGGCT	1501
Db	1690	TGCAAGTGTAGCAACCTGATTCGGTTGCTTCAACCTTAAAGCTTCAAGTCTTGGGCT	1749
Qy	1502	AAAATCGTATAAAAATCTGGATTTTTTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGAAACC	1561
Db	1750	AAAATCGTATAAAAATCTGGATTTTTTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGAAACC	1809
Qy	1562	AGAACATTTCTATGTACTACAAACCTGTTTAAAGGAGACTATGTCTGATCAATAA	1621
Db	1810	AGAACATTTCTATGTACTACAAACCTGTTTAAAGGAGACTATGTCTGATCAATAA	1869
Qy	1622	ACTTGTGTCRTGCTGATAGGACAGACTGGATTTTTTTTTCATATTTTCTTATTTAAATTTCTGCC	1681
Db	1870	ACTTGTGTCRTGCTGATAGGACAGACTGGATTTTTTTTTCATATTTTCTTATTTAAATTTCTGCC	1929
Qy	1682	ATTTAGAGAGAGAGACATACATTCATGTTTGGAGAGATTAACCTGAAAGAGAGTGG	1741
Db	1930	ATTTAGAGAGAGAGACATACATTCATGTTTGGAGAGATTAACCTGAAAGAGAGTGG	1989
Qy	1742	CTTATCTTCTACTTTATCGATAAGTCACTTATTTTGTGTTTCAATGTGTACATTTTATATT	1801
Db	1990	CTTATCTTCTACTTTATCGATAAGTCACTTATTTTGTGTTTCAATGTGTACATTTTATATT	2049
Qy	1802	CTTCTTTTGAATTAATACTGTTGGCTTTTCTAATCTTGTGTTTAAATATATCTATTTTACC	1861
Db	2050	CTTCTTTTGAATTAATACTGTTGGCTTTTCTAATCTTGTGTTTAAATATATCTATTTTACC	2109
Qy	1862	AAAGTATTTTAAATTTCTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGGTAAAT	1921
Db	2110	AAAGTATTTTAAATTTCTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGGTAAAT	2169
Qy	1922	TTTTCTAAACACAAATTTGTTATAGCCAGAGGAAACAGATGATATAAAATATTTGTGTC	1981
Db	2170	TTTTCTAAACACAAATTTGTTATAGCCAGAGGAAACAGATG---ATATAAATATTTGTGTC	2226
Qy	1982	CTGGACAAAAATACATGATATNTCCATCCGGAATGGTGTAGAGTTGGATTAACCTGCA	2041

Db 2227 TCTGACAAAATACATGTAATT-CAITCTCGTATGGTGTAGAGTTAGATT-AATCTGCA 2284
 QY 2042 TTTTAAAAAACCTGAATGGGAANGGAANTGGTAAGTTGGCCAAANCTTTTGTGAAA 2101
 Db 2285 TTTTAAAAAACCTGAATT---GGAATAGAAATGGTAAGTT---GCAAGACTTTTGTGAAA 2338

QY 2102 TAATTA 2108
 Db 2339 TAATTA 2345

RESULT 10

AA521386
 ID AA521386 standard; cDNA; 2849 BP.

XX
 AC AA521386;

DT 24-OCT-2001 (first entry)

XX Human cDNA sequence encoding for PRO200 polypeptide.

DE Human secretory and transmembrane; PRO; mammalian; cancer; lung;

XX breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;

KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;

KW adipocyte; A-peptide; factor VIIA; gene therapy; ss.

XX Homo sapiens.

XX WO200140466-A2.

XX 07-JUN-2001.

XX 01-DEC-2000; 2000WO-US32678.

XX 01-DEC-1999; 99WO-US28301.

XX 01-DEC-1999; 99WO-US28634.

XX 02-DEC-1999; 99WO-US28551.

XX 02-DEC-1999; 99WO-US28564.

XX 02-DEC-1999; 99WO-US28565.

XX 09-DEC-1999; 99US-0170262.

XX 16-DEC-1999; 99WO-US30095.

XX 20-DEC-1999; 99WO-US30911.

XX 20-DEC-1999; 99WO-US30999.

XX 30-DEC-1999; 99WO-US31243.

XX 06-JAN-2000; 2000WO-US00277.

XX 06-JAN-2000; 2000WO-US00376.

XX 11-FEB-2000; 2000WO-US03565.

XX 18-FEB-2000; 2000WO-US04341.

XX 18-FEB-2000; 2000WO-US04342.

XX 22-FEB-2000; 2000WO-US04414.

XX 24-FEB-2000; 2000WO-US04914.

XX 24-FEB-2000; 2000WO-US05004.

XX 01-MAR-2000; 2000WO-US05601.

XX 20-MAR-2000; 2000WO-US07377.

XX 21-MAR-2000; 2000WO-US07532.

XX 20-MAR-2000; 2000WO-US08439.

XX 17-MAY-2000; 2000WO-US13705.

XX 22-MAY-2000; 2000WO-US14042.

XX 30-MAY-2000; 2000WO-US14941.

XX 02-JUN-2000; 2000WO-US15264.

XX 10-NOV-2000; 2000WO-US30873.

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;

PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2001-408281/43.

DR P-PSDB; AAU12314.

XX Isolated, secretory and transmembrane PRO polypeptide used to detect

PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 XX
 PS Claim 3; Fig 285; 813pp; English.
 XX
 CC AAS21244-AAS21518 encode for novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 XX
 SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Query Match 93.9%; Score 1979.4; DB 22; Length 2849;

Best Local Similarity 97.7%; Pred. No. 0;

Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

QY 2 CCGCGCGTGGAGTCTCTCACCCAGTCAGCAAAATGAGCCTCTTCGGGCTTCCTGG 61
 Db 250 CCGCGCGTGGAGTCTCTCACCCAGTCAGCAAAATGAGCCTCTTCGGGCTTCCTGG 309
 QY 62 TGACATCTGCTGGCGGCCAGAGACGAGGAGCTCAGCGGAAATCCAACTGAGTAGTA 121
 Db 310 TGACATCTGCTGGCGGCCAGAGACGAGGAGCTCAGCGGAAATCCAACTGAGTAGTA 369
 QY 122 AATTCAGTTTCCAGCAACAGGACAGAGCGGAGTCAAGATCTCAGCATGAGAGAA 181
 Db 370 AATTCAGTTTCCAGCAACAGGACAGAGCGGAGTCAAGATCTCAGCATGAGAGAA 429
 QY 182 TTATTACTGTGTCTACTAATGGAATTTTCAGCGCCAAAGTTTCTCATCTTATCCAA 241
 Db 430 TTATTACTGTGTCTACTAATGGAATTTTCAGCGCCAAAGTTTCTCATCTTATCCAA 489
 QY 242 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATGTATGGATCAACTTA 301
 Db 490 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATGTATGGATCAACTTA 549
 QY 302 CGTTTGAATGAAGATTGGGCTTGAAGACCCAGAGAGATGACATATGCAAGTATGATTTTG 361
 Db 550 CGTTTGAATGAAGATTGGGCTTGAAGACCCAGAGAGATGACATATGCAAGTATGATTTTG 609
 QY 362 TAGAGTTGAGGAAACCCAGTATGAACTATATTAGGGCGCTGGTGTGTTCTGGTACTG 421
 Db 610 TAGAGTTGAGGAAACCCAGTATGAACTATATTAGGGCGCTGGTGTGTTCTGGTACTG 669
 QY 422 TACCAGGAAACAGATTTTCTAAGGAAATCAAAATAGGATAGATTTGTATCTGATGAT 481
 Db 670 TACCAGGAAACAGATTTTCTAAGGAAATCAAAATAGGATAGATTTGTATCTGATGAT 729
 QY 482 ATTTTCTTCTGAACCCAGGGTTCTGCATCTCCACTACAACTTCTATGCCACAATTCACAG 541
 Db 730 ATTTTCTTCTGAACCCAGGGTTCTGCATCTCCACTACAACTTCTATGCCACAATTCACAG 789
 QY 542 AAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGCCACTGACCTGCTTAATATG 601
 Db 790 AAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGCCACTGACCTGCTTAATATG 849

602	QY	CTATAACTGCGCTTTAGTACTCTGGAAAGACCTTATTTCGATATCTCTCAACCGAGAGATGCG	661
850	DB	CTATAACTGCGCTTTAGTACTCTGGAAAGACCTTATTTCGATATCTTGGAAACGAGAGATGCG	909
662	QY	AGTTGGACTTTAGAAGATCTATATAGGCCAACTTGGCAACTCTCTGGCAAGGCTTTTGT	721
910	DB	AGTTGGACTTTAGAAGATCTATATAGGCCAACTTGGCAACTCTCTGGCAAGGCTTTTGT	969
722	QY	TTTGGAGAAAATCCAGAGTGTGGATCTGAACCTTCTAACAGAGAGAGTGAAGATTATACA	781
970	DB	TTTGGAGAAAATCCAGAGTGTGGATCTGAACCTTCTAACAGAGAGAGTGAAGATTATACA	1029
782	QY	GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCA	841
1030	DB	GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCA	1089
842	QY	TTTTCTGGCCAGGTTGTCTCTCGTTTAAACGCTGTGGTGGGAACCTGTGCTGTGTCTCTCC	901
1090	DB	TTTTCTGGCCAGGTTGTCTCTCGTTTAAACGCTGTGGTGGGAACCTGTGCTGTGTCTCTCC	1149
902	QY	ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTTAAATAACACGAGGTCC	961
1150	DB	ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTTAAATAACACGAGGTCC	1209
962	QY	TTTCAGTTGAGACCAAGACCGGTGTCCAGGGGATTGCACAAATCACTCACCGACGTGGCC	1021
1210	DB	TTTCAGTTGAGACCAAGACCGGTGTCCAGGGGATTGCACAAATCACTCACCGACGTGGCC	1269
1022	QY	TGGAGCAACATGAGGAGTGTGACTGTGTGTGCAGAGGAGACACAGAGGATACCGCATC	1081
1270	DB	TGGAGCAACATGAGGAGTGTGACTGTGTGTGCAGAGGAGACACAGAGGATACCGCATC	1329
1082	QY	ACCACACAGACGCTCTTTGCCACAGACGTGTGCAGTGCAGTGGCTGATTTCTATTAGAGAACGT	1141
1330	DB	ACCACACAGACGCTCTTTGCCACAGACGTGTGCAGTGCAGTGGCTGATTTCTATTAGAGAACGT	1389
1142	QY	ATGCGTTATCTCATCCTTAACTCAGTTGTTTTCCTTCAAGACCTTTTCATCTTCAGGAT	1201
1390	DB	ATGCGTTATCTCATCCTTAACTCAGTTGTTTTCCTTCAAGACCTTTTCATCTTCAGGAT	1449
1202	QY	TTACAGTGCATCTGAAAGAGGAGACATCAAAACAGAAATTAGAGTTGTGCAACAGCTCTT	1261
1450	DB	TTACAGTGCATCTGAAAGAGGAGACATCAAAACAGAAATTAGAGTTGTGCAACAGCTCTT	1509
1262	QY	TTGAGAGAGGCGCTTAAAGACAGGAGAAAAGTCTTCAATCGTGGAAAGAAAATTAAATG	1321
1510	DB	TTGAGAGAGGCGCTTAAAGACAGGAGAAAAGTCTTCAATCGTGGAAAGAAAATTAAATG	1569
1322	QY	TTGTATTAAATAGATCACCAGCTAGTTTTCAGAGTTTACCATGTACGTATTCCACTAGCTGG	1381
1570	DB	TTGTATTAAATAGATCACCAGCTAGTTTTCAGAGTTTACCATGTACGTATTCCACTAGCTGG	1629
1382	QY	GTCTCTGATTTTCAGTTCTTTTCGATACGGCTTAGGTGAATGTCCAGTACAGGAAAACCTG	1441
1630	DB	GTCTCTGATTTTCAGTTCTTTTCGATACGGCTTAGGTGAATGTCCAGTACAGGAAAACCTG	1689
1442	QY	TGCAAGTGAGCACCTGATTCCGTTGCTTGTCTTAACTCTAAAGCTCCATGTCTCTGGCGCT	1501
1690	DB	TGCAAGTGAGCACCTGATTCCGTTGCTTGTCTTAACTCTTAAAGCTCCATGTCTCTGGCGCT	1749
1502	QY	AAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTACATGTATAAC	1561
1750	DB	AAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTACATGTATAAC	1809
1562	QY	AGAACATTCCTATGTACTACAAACCTGGTTTTTAAAAAGGAACCTATGTGCTATGAATTAA	1621
1810	DB	AGAACATTCCTATGTACTACAAACCTGGTTTTTAAAAAGGAACCTATGTGCTATGAATTAA	1869
1622	QY	ACTGTGTGTCTGTGTATAGACAGCTGGATTTTTTTCATATTCTTCTTATTAATAATTTCTGCC	1681
1870	DB	ACTGTGTGTCTGTGTATAGACAGCTGGATTTTTTTCATATTCTTCTTATTAATAATTTCTGCC	1929
1682	QY	ATTTAGAAGAGAGAACTACAATTATGTTTGGAAAGAGATAAACTCTGAAAGAGAGTGG	1741


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1870 ACTTGTGTCATGCTGATAGCAGACAGCTGGATTTTTCATATTTCTTATTAATAATTTCTGCC 1929
1882 ATTTAGAGAGAGAACTACATTCATGGTTTGGAGAGATAAACCTGAAAGAGAGTGG 1741
1930 ATTTAGAGAGAGAACTACATTCATGGTTTGGAGAGATAAACCTGAAAGAGAGTGG 1989
1742 CTTATCTTCACCTTATCGATAGTCAGTTTATTTGTTTCATTTGTTGATACATTTTATATT 1801
1990 CCTTATCTTCACCTTATCGATAGTCAGTTTATTTGTTTCATTTGTTGATACATTTTATATT 2049
1802 CTCCTTTTGCATTAATACTGTTGGCTTTCTAATCTTCTGTAATAATATATCTATTTTACC 1861
2050 CTCCTTTTGCATTAATACTGTTGGCTTTCTAATCTTCTGTAATAATATATCTATTTTACC 2109
1862 AAGGTATTAATATCTTTTATGACAACTTAGATCAACTATTTTTHAGCTGGTAAAT 1921
2110 AAGGTATTAATATCTTTTATGACAACTTAGATCAACTATTTTTHAGCTGGTAAAT 2169
1922 TTTTCTAAACACAAATGTTTATAGCCAGAGAAACAAAGATGGATATAAAATATTTGTTGC 1981
2170 TTTTCTAAACACAAATGTTTATAGCCAGAGAAACAAAGATGGATATAAAATATTTGTTGC 2226
1982 CTGACAAATAACATGTTATNTCCATCCCGGAATGGTGTAGAGTTGGATTAAACCTGCA 2041
2227 TCTGACAAATAACATGTTATTT-CATCTCGTATGGTGTAGAGTTAGATT-AACTGCA 2284
2042 TTTTAAACAACTGTAATGGGAGGAANTTGTGAAGTTGGCCAAACCTTTTGGAAA 2101
2285 TTTTAAACAACTGTAATGGGAGGAANTTGTGAAGTTGGCCAAACCTTTTGGAAA 2338
2102 TAATTAA 2108
2339 TAATTAA 2345

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RESULT 12

AAC88962
ID AAC88962 standard; cdna; 2849 BP.

AC AAC88962;

XX 06-MAR-2001 (first entry)

DT Human PRO200 coding sequence.

XX Human; PRO526; PRO719; PRO200; PRO725; PRO1031; immune related disease;
inflammation; thyroiditis; demyelinating disease; skin disease;
XX infectious disease; ss.

OS Homo sapiens.

XX WO200070050-A1.

XX 23-NOV-2000.

XX 21-MAR-2000; 2000WO-US07532.

XX 14-MAY-1999; 99US-0134287.

XX (GETH) GENENTECH INC.

XX Baker KP, Chen J, Ferrara N, Fong S, Goddard A, Gurney AL;

XX Hillan KJ, Kuo SS, Tumas D, Wood WI;

XX WPI; 2001-025022/03.

XX P-PSDB; AAB49895.

XX New compositions containing a PRO526, PRO719, PRO725, PRO1031 or PRO200
PT proteins for modulating immune response or proliferation of
PT T-lymphocytes in mammal, especially for treating immune related
PT disorders, e.g. graft rejection -

XX

PS Claim 21; Fig 9; 133pp; English.

XX The present invention discloses the coding and protein sequences of human
CC proteins PRO526, PRO719, PRO725, PRO1031 and PRO200. These proteins, of
CC their coding sequences and antibodies can be used in the treatment of
CC immune-related diseases, including systemic lupus erythematosus,
CC rheumatoid arthritis, thyroiditis, immune-mediated renal disease,
CC demyelinating diseases such as multiple sclerosis, hepatobiliary diseases
CC including primary biliary cirrhosis, inflammatory bowel disease,
CC immune-mediated skin diseases such as psoriasis, allergic diseases
CC including asthma, immunologic diseases of the lung, transplantation
CC associated diseases and infectious diseases such as HIV and hepatitis.

SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Query Match 93.9%; Score 1979.4; DB 22; Length 2849;

Best Local Similarity 97.7%; Pred. No. 0;

Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

QY 2 CCCGCGGTGAGTCTCTCACCCAGTCAGCCCAATGAGCCTCTTCGGGCTTCTCCTGG 61

DB 250 CCCGCGGTGAGTCTCTCACCCAGTCAGCCCAATGAGCCTCTTCGGGCTTCTCCTGC 309

QY 62 TGACATCTGCCTGCGCGGCCAGAGAGAGGGAATCTAGGCGGAATCCAACTGATGATA 121

DB 310 TGACATCTGCCTGCGCGGCCAGAGAGAGGGAATCTAGGCGGAATCCAACTGATGATA 369

QY 122 AATTCAGATTTTCAGGCAACAAAGGACAGACGAGGATCTAGGCGGAATCCAACTGATGATA 181

DB 370 AATTCAGATTTTCAGGCAACAAAGGACAGACGAGGATCTAGGCGGAATCCAACTGATGATA 429

QY 182 TTATTACTGTCTACTAATGGAAGTATTCACGCCCAAGGTTTCTCATATCTTATCCAA 241

DB 430 TTATTACTGTCTACTAATGGAAGTATTCACGCCCAAGGTTTCTCATATCTTATCCAA 489

QY 242 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGATGGATACAACTTA 301

DB 490 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGATGGATACAACTTA 549

QY 302 CGTTTGATGAAGATTTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTG 361

DB 550 CGTTTGATGAAGATTTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTG 609

QY 362 TAGAAGTTGAGAAACCCAGTGTATTAATGAGGCGCTGCTGGTGGTCTGGTACTG 421

DB 610 TAGAAGTTGAGAAACCCAGTGTATTAATGAGGCGCTGCTGGTGGTCTGGTACTG 669

QY 422 TACCAGGAAACACAGATTTCTAAAGGAATCAAAATTTAGGATAAGATTTGTATCTGATGAAT 481

DB 670 TACCAGGAAACACAGATTTCTAAAGGAATCAAAATTTAGGATAAGATTTGTATCTGATGAAT 729

QY 482 ATTTTCTCTTGAACCCAGGTTTCTGCATCCACTACAACATTTGTATGCCCAATTCACAG 541

DB 730 ATTTTCTCTTGAACCCAGGTTTCTGCATCCACTACAACATTTGTATGCCCAATTCACAG 789

QY 542 AAGCTGTGAGTCTTCACTGCTACCCCTTTCAGCTTTCGCACTGGACCTGTTTAATG 601

DB 790 AAGCTGTGAGTCTTCACTGCTACCCCTTTCAGCTTTCGCACTGGACCTGTTTAATG 849

QY 602 CTATAACTGCTTTTAGTACCTTGGAGACCTTATTCGATATCTTGAACCCAGAGATGGC 661

DB 850 CTATAACTGCTTTTAGTACCTTGGAGACCTTATTCGATATCTTGAACCCAGAGATGGC 909

QY 662 AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTGTTT 721

DB 910 AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTGTTT 969

QY 722 TTGAGAGAAATCCAGAGTGGTGTGATCTGAACCTTCTAAACAGAGAGGTAAATATACA 781

DB 970 TTGAGAGAAATCCAGAGTGGTGTGATCTGAACCTTCTAAACAGAGAGGTAAATATACA 1029

QY 782 GCTGCACACCTTCGTAACCTTCTCAGTGTCTCAATAGGAGAACTAAAGAGAACCGATACCA 841

XX PS Claim 58; Fig 21A-B; 293pp; English.

XX CC The invention relates to novel human angiogenesis-associated proteins

CC designated PRO proteins (AA853064-B53097), and to nucleic acids encoding

CC PRO proteins. The invention also relates to vectors and host cells

CC comprising a PRO nucleic acid, the recombinant production of a PRO

CC protein, PRO antibodies specific for a PRO protein, fusion proteins

CC comprising a PRO protein, agonists or antagonists of a PRO protein, and

CC compounds which inhibit the expression of a PRO gene. The invention

CC additionally encompasses methods of identifying modulators of PRO

CC expression or activity; diagnosing a cardiovascular, endothelial or

CC angiogenic disorder, or a susceptibility to such a disorder by detecting

CC mutations in a PRO gene, or the expression level of a PRO gene within a

CC particular tissue; treating a cardiovascular, endothelial or angiogenic

CC disorder via the administration of a PRO protein, PRO nucleic acid, or

CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a

CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial

CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the

CC administration of a PRO protein, or an agonist or antagonist thereof.

CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO

CC agonists and PRO antagonists may be used as therapeutic agents to treat

CC cardiovascular, endothelial or angiogenic disorders, such as

CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,

CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,

CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's

CC disease, or stroke. PRO nucleic acids are additionally useful in the

CC recombinant production of PRO proteins, as hybridisation probes to

CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,

CC to map genes encoding PRO proteins, to analyse genetic disorders, and in

CC gene therapy. PRO nucleic acids can also be used to produce transgenic

CC animals useful for the development and screening of potential

CC therapeutic agents. The present sequence represents a cDNA encoding a PRO

CC protein of the invention.

XX SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Query Match 93.9%; Score 1979.4; DB 22; Length 2849;

Best Local Similarity 97.7%; Pred. No. 0;

Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

QY 2 CCGCCGTGAGCTCTCACCCAGTCAGCCCAATGAGCTCTTCGGGCTTCCTCG 61

DB 250 CCGCCGTGAGCTCTCACCCAGTCAGCCCAATGAGCTCTTCGGGCTTCCTCG 309

QY 62 TGACATCTGCCCTGGCCGCGCAGAGACAGGGGACTCAGCGGGAATCAACCTGAGTAGTA 121

DB 310 TGACATCTGCCCTGGCCGCGCAGAGACAGGGGACTCAGCGGGAATCAACCTGAGTAGTA 369

QY 122 AATTCAGTTTTCCAGCAACAGGACAGACCGAGTACAGATCTCTCAGCATGAGAGAA 181

DB 370 AATTCAGTTTTCCAGCAACAGGACAGACCGAGTACAGATCTCTCAGCATGAGAGAA 429

QY 182 TTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCTACTATTCCAA 241

DB 430 TTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCTACTATTCCAA 489

QY 242 GAAATACGGTCTTGATGAGATAGTAGCAGTACAGGAAATGATGAGTACAACTTA 301

DB 490 GAAATACGGTCTTGATGAGATAGTAGCAGTACAGGAAATGATGAGTACAACTTA 549

QY 302 CGTTTGATGAAGATTTGGGCTTGAGACCCAGAGATGACATATCAGATGATGATTTTG 361

DB 550 CGTTTGATGAAGATTTGGGCTTGAGACCCAGAGATGACATATCAGATGATGATTTTG 609

QY 362 TAGAAGTTGAGGAACCCAGTGATGGAATATATTAGGGCGCTGGTGGTCTCTGGTACTG 421

DB 610 TAGAAGTTGAGGAACCCAGTGATGGAATATATTAGGGCGCTGGTGGTCTCTGGTACTG 669

QY 422 TACCAGGAACAGATTTCTTAAGGAATCAAAATTAGGATAGATTTGATCTGATGAAT 481

DB 670 TACCAGGAACAGATTTCTTAAGGAATCAAAATTAGGATAGATTTGATCTGATGAAT 729

QY 482 ATTTTCCTTCTGAACACGGGTTCTGCATCCACTACACATTGTCTCATGCCACAATTCCAG 541

DB 730 ATTTTCCTTCTGAACACGGGTTCTGCATCCACTACACATTGTCTCATGCCACAATTCCAG 789

QY 542 AAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGCCACTGGAACTGCTTAAATAG 601

DB 790 AAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGCCACTGGAACTGCTTAAATAG 849

QY 602 CTATAACGCTTTAGTACCTTTGAAGACCTTATTCGATATCTTGAACACAGAGATGGC 661

DB 850 CTATAACGCTTTAGTACCTTTGAAGACCTTATTCGATATCTTGAACACAGAGATGGC 909

QY 662 AGTTGGACTTGAAGATCTATATAGGCCAACTTCGGCAACTTCTTGGCAAGGCTTTTGT 721

DB 910 AGTTGGACTTGAAGATCTATATAGGCCAACTTTGGCAACTTCTTGGCAAGGCTTTTGT 969

QY 722 TTGAAGAAATCCAGAGTGTGATCTGAACCTTTCTAACAGAGAGAGTAAATATACA 781

DB 970 TTGAAGAAATCCAGAGTGTGATCTGAACCTTTCTAACAGAGAGAGTAAATATACA 1029

QY 782 GCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAGAACTAAAGAGAACCGATACA 841

DB 1030 GCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAGAACTAAAGAGAACCGATACA 1089

QY 842 TTTTCGCGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGAACTGTGCTGTGTCTCC 901

DB 1090 TTTTCGCGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGAACTGTGCTGTGTCTCC 1149

QY 902 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAGTACTTAAATAATACCACAGGCTCC 961

DB 1150 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAGTACTTAAATAATACCACAGGCTCC 1209

QY 962 TTCAGTTCAGACCAAGAACCGGTGTCAAGGGATTTGCAAAATCACTACCCAGCTGGGCC 1021

DB 1210 TTCAGTTCAGACCAAGAACCGGTGTCAAGGGATTTGCAAAATCACTACCCAGCTGGGCC 1269

QY 1022 TGGAGACCATGAGAGTGTGACTGTGTGCGAGGGAGACAGAGGATAGCGGCATC 1081

DB 1270 TGGAGACCATGAGAGTGTGACTGTGTGCGAGGGAGACAGAGGATAGCGGCATC 1329

QY 1082 ACCACCCAGCTCTTCCAGAGCTGTGAGTGTGCGAGGGAGACAGAGGATAGCGGCATC 1141

DB 1330 ACCACCCAGCTCTTCCAGAGCTGTGAGTGTGCGAGGGAGACAGAGGATAGCGGCATC 1389

QY 1142 ATGGCTTATCTCCATCTTAACTCTCAGTGTGTTTGGTTCGAAGGACCTTTCATCTTCAG 1201

DB 1390 ATGGCTTATCTCCATCTTAACTCTCAGTGTGTTTGGTTCGAAGGACCTTTCATCTTCAG 1449

QY 1202 TTACAGTGCATCTGAAAGAGAGACATCAAAACAGAAATTAGAGTTGTGCAACAGCTCTT 1261

DB 1450 TTACAGTGCATCTGAAAGAGAGACATCAAAACAGAAATTAGAGTTGTGCAACAGCTCTT 1509

QY 1262 TTGAGAGAGGCTTAAAGGACAGGAGAAAGGCTTCTCAATCGTGAAGAGAAATTAATG 1321

DB 1510 TTGAGAGAGGCTTAAAGGACAGGAGAAAGGCTTCTCAATCGTGAAGAGAAATTAATG 1569

QY 1322 TTGATTAATAATAGATCAACAGCTAGTTTCAGAGTTACCATGTACATATTCACATAGCTGG 1381

DB 1570 TTGATTAATAATAGATCAACAGCTAGTTTCAGAGTTACCATGTACATATTCACATAGCTGG 1629

QY 1382 GTTCTGTATTTTCAGTCTTTCGATACGGCTTAGGGTATGTGCTACAGGAGAAACCTG 1441

DB 1630 GTTCTGTATTTTCAGTCTTTCGATACGGCTTAGGGTATGTGCTACAGGAGAAACCTG 1689

QY 1442 TGCAGTGAACCTGATTCGGTTTGCCTTGTCTTAACTCTAAAGCTCCATGCTCTGGGCT 1501

DB 1690 TGCAGTGAACCTGATTCGGTTTGCCTTGTCTTAACTCTAAAGCTCCATGCTCTGGGCT 1749

QY 1502 AAAATCGTATAAATCTGGATTTTTTTTTTTTTTTTTTTTTTTTTTCTCATATTCATATAACC 1561

DB 1750 AAAATCGTATAAATCTGGATTTTTTTTTTTTTTTTTTTTTTTTTTCTCATATTCATATAACC 1809

QY 1562 AGAATCTCTATGACTACAAACCTGGTTTTTTTTAAAAAGGAACATATGTTGCTATGAATTA 1621

PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 PA (GETH) GENENTECH INC.
 XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-332040/31.
 DR P-PSDB; ABU66712.
 XX
 PT New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping, as chromosome markers, in
 PT tissue typing, and in chromosome identification -
 XX
 PS Claim 2; Fig 285; 660pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists.
 CC The PRO polypeptides are useful for stimulating the release of
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating
 CC the proliferation or differentiation of chondrocytes, and detecting the
 CC presence of tumours. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and
 CC gene mapping, in the generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptides, for generating transgenic animals or
 CC knockout animals, for the genetic analysis of individuals with genetic
 CC disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
 CC encoding the human PRO polypeptides of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipsdIDentry.html.
 XX
 SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;
 Query Match 93.9%; Score 1979.4; DB 25; Length 2849;
 Best Local Similarity 97.7%; Pred. No. 0;
 Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;
 QY 2 CCCGCCGTGAGTGAGCTCTCACCCAGTCAGCCCAATGAGCCTCTTGGGCTTCTCTGG 61
 DB 250 CCCGCCGTGAGTGAGCTCTCACCCAGTCAGCCCAATGAGCCTCTTGGGCTTCTCTGC 309
 QY 62 TGACATCTGCCCTGCCGCGCAGAGCAGGGGCTCAGCGGATCCCACTCAGTAGTA 121
 DB 310 TGACATCTGCCCTGCCGCGCAGAGCAGGGGCTCAGCGGATCCCACTCAGTAGTA 369
 QY 122 AATTCAGATTTTCCAGCAACAAGCAACAGGAGTACAGATCTCTCAGCATGAGAGAA 181
 DB 370 AATTCAGATTTTCCAGCAACAAGCAACAGGAGTACAGATCTCTCAGCATGAGAGAA 429
 QY 182 TTATTACTGTGCTTACTAATGGAAGTATTACAGCCCAAGGTTTCTCTACTATTACCAA 241
 DB

DB 430 TTATTACTGTGCTTACTAATGGAAGTATTACAGCCCAAGGTTTCTCTACTATTACCAA 489
 QY 242 GAAATACCGTCTTGGTATGAGATTTAGCAGTAGAGGAAAAATGTATGGATACAACTTA 301
 DB 490 GAAATACCGTCTTGGTATGAGATTTAGCAGTAGAGGAAAAATGTATGGATACAACTTA 549
 QY 302 CGTTTGATGAAGATTTGGGCTTCAGAGACCAGAGAGATGACATATGCAAGTATGATTTG 361
 DB 550 CGTTTGATGAAGATTTGGGCTTCAGAGACCAGAGAGATGACATATGCAAGTATGATTTG 609
 QY 362 TAGAAGTTGAGAAACCCAGTGTGAACTATATTAGGCGCTGTGTGGTTCTCGTACTG 421
 DB 610 TAGAAGTTGAGAAACCCAGTGTGAACTATATTAGGCGCTGTGTGGTTCTCGTACTG 669
 QY 422 TACCAGGAAACAGATTTCTAAGGGAATCAAAATAGGATAGATTTGTATCTCATGAAT 481
 DB 670 TACCAGGAAACAGATTTCTAAGGGAATCAAAATAGGATAGATTTGTATCTCATGAAT 729
 QY 482 ATTTTCTCTTGAACACAGGTTTCTGATCCACTACCAATTTGTCTCATGCAAAATTCACAG 541
 DB 730 ATTTTCTCTTGAACACAGGTTTCTGATCCACTACCAATTTGTCTCATGCAAAATTCACAG 789
 QY 542 AAGCTGTGAGTCTTTCAGTGTACCCCTTCAGCTTTGCCACTGCACTGCTTTAATG 601
 DB 790 AAGCTGTGAGTCTTTCAGTGTACCCCTTCAGCTTTGCCACTGCACTGCTTTAATG 849
 QY 602 CTATAACTGCCCTTTAGTACCTTTGGAAGACCTTATTTCGATATCTTGAACACAGAGATGGC 661
 DB 850 CTATAACTGCCCTTTAGTACCTTTGGAAGACCTTATTTCGATATCTTGAACACAGAGATGGC 909
 QY 662 AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGT 721
 DB 910 AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGT 969
 QY 722 TTGGAGAAATCCAGTGTGTGATCTGACCTTCTAACAGAGGAGGTAGATATACA 781
 DB 970 TTGGAGAAATCCAGTGTGTGATCTGACCTTCTAACAGAGGAGGTAGATATACA 1029
 QY 782 GCTGCACACCTCGTAACTCTTCAAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACA 841
 DB 1030 GCTGCACACCTCGTAACTCTTCAAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACA 1089
 QY 842 TTTTCTGGCCAGGTTGTCTCTGTTAAACGCTGTGTGGGAACTGTGCTCTGTGTCTCC 901
 DB 1090 TTTTCTGGCCAGGTTGTCTCTGTTAAACGCTGTGTGGGAACTGTGCTCTGTGTCTCC 1149
 QY 902 ACAATTCGAATGAATGTCAATGTGTCCCAAGCAAAATTTACTAAAAAATACCAAGAGTCC 961
 DB 1150 ACAATTCGAATGAATGTCAATGTGTCCCAAGCAAAATTTACTAAAAAATACCAAGAGTCC 1209
 QY 962 TTCAGTTGAGACCAAAAGACCGGTGTGAGGGATGTCACAAATCACTACCGAGTGGGCC 1021
 DB 1210 TTCAGTTGAGACCAAAAGACCGGTGTGAGGGATGTCACAAATCACTACCGAGTGGGCC 1269
 QY 1022 TCGAGCACCATGAGGAGTGTGACTGTGTGCAGAGGAGCAGAGGAGTAGCCGATC 1081
 DB 1270 TCGAGCACCATGAGGAGTGTGACTGTGTGCAGAGGAGCAGAGGAGTAGCCGATC 1329
 QY 1082 ACCACACGAGCTCTTGTCCAGAGCTGTGCAAGTGTGAGTGTGATTTCTATTAGAGAACGT 1141
 DB 1330 ACCACACGAGCTCTTGTCCAGAGCTGTGCAAGTGTGAGTGTGATTTCTATTAGAGAACGT 1389
 QY 1142 ATGCGTTATCTCCATCTTAATCTCAGTTGTTCTTCAAGGACCTTCTCTCAGGAT 1201
 DB 1390 ATGCGTTATCTCCATCTTAATCTCAGTTGTTCTTCAAGGACCTTCTCTCAGGAT 1449
 QY 1202 TTACAGTGTCTTGAAGAGGAGACATCAAAAGAAATTAGAGTTGTGCAACAGCTCTT 1261
 DB 1450 TTACAGTGTCTTGAAGAGGAGACATCAAAAGAAATTAGAGTTGTGCAACAGCTCTT 1509
 QY 1262 TTGAGAGGAGGCTTAAAGGACAGGAGAAAGGCTTCTCAATCGTGGAAGAAAAATTAATG 1321
 DB 1510 TTGAGAGGAGGCTTAAAGGACAGGAGAAAGGCTTCTCAATCGTGGAAGAAAAATTAATG 1569

PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 23-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19592.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
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 PR 28-FEB-2001; 2001US-0796498.
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 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX
 PA (SETH) GENENTECH INC.
 XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI: 2003-331925/31.
 DR P-PSDB: ABU66988.
 XX
 FT New secreted and transmembrane nucleic acids and polypeptides,
 PT designated as PRO, useful for treating inflammation, organ failure,
 PT atherosclerosis, cardiac injury, infertility, birth defects, premature
 PT aging, AIDS, or cancer
 XX
 PS Claim 2; Fig 285; 659pp; English.

XX The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid
 CC further comprises the full-length coding sequence of the DNA deposited
 CC under American Type Culture Collection (ATCC) accession number in a list
 CC given in the specification. Also included are vectors and host
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
 CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of
 CC TNF-alpha (tumor necrosis factor alpha) from human blood,
 CC (and the proliferation of differentiation of chondrocyte cells, the
 CC proliferation of, or gene expression in pericyte cells, the release or
 CC proteoglycans from cartilage, proliferation of inner ear articular
 CC supporting cells, the proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
 CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC a method for inhibiting the binding of A-peptide to factor VIIA,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumour in a mammal and an oligonucleotide probe derived

CC from any of the nucleotide sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridisation
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence encodes a PRO protein of the invention.

XX SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Query Match 93.9%; Score 1979.4; DB 25; Length 2849;

Best Local Similarity 97.7%; Pred. No. 0;

Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

QY 2 CCGCCGCTGAGTGAGCTCTCACCCGAGTCAGCCAAATGAGGCTCTTGGGGTTCTCTCTGG 61
 DB 250 CCGCCGCTGAGTGAGCTCTCACCCGAGTCAGCCAAATGAGGCTCTTGGGGTTCTCTCTGG 309
 QY 62 TGACATCTGCCCTGGCCGCGCAGAGACGAGGAGCTCAGGCGGAATCCAACTGAGTAGTA 121
 DB 310 TGACATCTGCCCTGGCCGCGCAGAGACGAGGAGCTCAGGCGGAATCCAACTGAGTAGTA 369
 QY 122 AATCCAGTTTTCAGCAACCAAGGAACAGAACGAGATCAAGATCCTCAGCATGAGAGAA 181
 DB 370 AATCCAGTTTTCAGCAACCAAGGAACAGAACGAGATCAAGATCCTCAGCATGAGAGAA 429
 QY 182 TTATTACTGTCTTACTAATCGAAGTATTCACGCCCAAGGTTTCTCATACTTATCCAA 241
 DB 430 TTATTACTGTCTTACTAATCGAAGTATTCACGCCCAAGGTTTCTCATACTTATCCAA 489
 QY 242 GAAATACGGTCTTGGTATGAGATTTAGTAGCAGTAGAGAGAAATGTATGATACAACTTA 301
 DB 490 GAAATACGGTCTTGGTATGAGATTTAGTAGCAGTAGAGAGAAATGTATGATACAACTTA 549
 QY 302 CGTTTGATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTG 361
 DB 550 CGTTTGATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTG 609
 QY 362 TAGAAGTTGAGAACCCAGTGTATGAACTATATTAGGGCGCTGGTGTGGTCTGGTACTG 421
 DB 610 TAGAAGTTGAGAACCCAGTGTATGAACTATATTAGGGCGCTGGTGTGGTCTGGTACTG 669
 QY 422 TACAGGAAAAACAGATTTCTTAAAGAAATCAAAATTAGGATTAAGATTTGTATCTGATGAAT 481
 DB 670 TACAGGAAAAACAGATTTCTTAAAGAAATCAAAATTAGGATTAAGATTTGTATCTGATGAAT 729
 QY 482 ATTTTCTTCTGAAACCGGGTTCTGCATCCACTCAACATTTGTCATGCCCAATTCACAG 541
 DB 730 ATTTTCTTCTGAAACCGGGTTCTGCATCCACTCAACATTTGTCATGCCCAATTCACAG 789
 QY 542 AAGCTGTGAGTCTTCTCAGTGTACCCCTTCAGCTTTGCCACTGCCACTGCTGCTTAATATG 601
 DB 790 AAGCTGTGAGTCTTCTCAGTGTACCCCTTCAGCTTTGCCACTGCCACTGCTGCTTAATATG 849
 QY 602 CTATACTGCTCTTAGTACTTGGAGACCTTATTCGATATCTTGAACACGAGAGATGGC 661
 DB 850 CTATACTGCTCTTAGTACTTGGAGACCTTATTCGATATCTTGAACACGAGAGATGGC 909
 QY 662 AGTTGGACTTAGAAGATCTATATAGGCCCACTTGGCAACTTCTTGGCAAGGCTTTTGT 721
 DB 910 AGTTGGACTTAGAAGATCTATATAGGCCCACTTGGCAACTTCTTGGCAAGGCTTTTGT 969
 QY 722 TTGGAAGAAATCCAGATGTTGATCTGAACCTTCTAAACAGAGAGATTAAGATTAACA 781
 DB 970 TTGGAAGAAATCCAGATGTTGATCTGAACCTTCTAAACAGAGAGATTAAGATTAACA 1029
 QY 782 GCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAGAGACTAAAGAGACCGATACCA 841
 DB 1030 GCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAGAGACTAAAGAGACCGATACCA 1089
 QY 842 TTTTCTGCCAGGTTGTCTCTCTGGTTAAACCGCTGTGGTGGGAACGTGTGCTGTGTCTCC 901

Db 1090 TTTTCTGGCCAGGTGTCTCTGGTTAAACGCTGTGTGGAACTGTGCTGTGTCTCC 1149
QY 902 ACAATTCGAATGAATGTCAATGTCTCCCAAGCAAAAGTTACTTAAATAATACCAAGAGTCC 961
Db 1150 ACAATTCGAATGAATGTCAATGTCTCCCAAGCAAAAGTTACTTAAATAATACCAAGAGTCC 1209
QY 962 TTCAGTTGAGACCAAGACCGGTGTGAGGGATTCGCAATCACTCACCGAGCGTGGCC 1021
Db 1210 TTCAGTTGAGACCAAGACCGGTGTGAGGGATTCGCAATCACTCACCGAGCGTGGCC 1269
QY 1022 TGGAGCACCATGAGAGGTGTCACTGTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGCATC 1081
Db 1270 TGGAGCACCATGAGAGGTGTCACTGTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGCATC 1329
QY 1082 ACCACCAGACGCTTGGCCAGAGCTGTGCACTGAGTGGCTGATTTCTATTAGAACGT 1141
Db 1330 ACCACCAGACGCTTGGCCAGAGCTGTGCACTGAGTGGCTGATTTCTATTAGAACGT 1389
QY 1142 ATGGTTATCTCCATCTTAATCTCAGTTGTGTGCTTCAAGSACCTTTTCATCTTCAGGAT 1201
Db 1390 ATGGTTATCTCCATCTTAATCTCAGTTGTGTGCTTCAAGSACCTTTTCATCTTCAGGAT 1449
QY 1202 TTACAGTGCATCTGAAGAGGAGACATCAACAGAAATTAGAGTTGTGCAACAGCTCTT 1261
Db 1450 TTACAGTGCATCTGAAGAGGAGACATCAACAGAAATTAGAGTTGTGCAACAGCTCTT 1509
QY 1262 TTGAGAGGAGGCTTAAAGGACAGAGAAAGGCTTCAATCGTGGAAAGAAATTAATG 1321
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QY 1322 TTGATTAATAATAGATCACAGTAGTTTCAGAGTTACCAAGTACGATTCACAGTAGCTGG 1381
Db 1570 TTGATTAATAATAGATCACAGTAGTTTCAGAGTTACCAAGTACGATTCACAGTAGCTGG 1629
QY 1382 GTTCTGTATTTTCAGTTCTTTCGATACGGCTTAGGTAAATGTCAGTACAGGAAAAAACTG 1441
Db 1630 GTTCTGTATTTTCAGTTCTTTCGATACGGCTTAGGTAAATGTCAGTACAGGAAAAAACTG 1589
QY 1442 TGCAGTGAGCACCTGATTCGGTTGCTTGTCTTAACCTAAAGCTCCATGTCCTGGGCT 1501
Db 1690 TGCAGTGAGCACCTGATTCGGTTGCTTGTCTTAACCTAAAGCTCCATGTCCTGGGCT 1749
QY 1502 AAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGTAACC 1561
Db 1750 AAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGTAACC 1809
QY 1562 AGAACATTTCTATGTACTACAAACCTGGTTTTTAAAGGAACCTATGTTGCTATGAATTA 1621
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QY 1622 ACTTGTGTCRTGCTGATAGGACAGACTGATTTTTTCATATTTCTATTAAATTTCTGCC 1681
Db 1870 ACTTGTGTCRTGCTGATAGGACAGACTGATTTTTTCATATTTCTATTAAATTTCTGCC 1929
QY 1682 ATTTAGAAGAGAGAACTACATTCATGTTTGGAGAGATAAACCTGAAAGAGAGAGTGG 1741
Db 1930 ATTTAGAAGAGAGAACTACATTCATGTTTGGAGAGATAAACCTGAAAGAGAGAGTGG 1989
QY 1742 CTTTATCTTCACTTTATCGATAAGTCACTTTATTTGTTTCACTTGTGTCATTTTTATTT 1801
Db 1990 CTTTATCTTCACTTTATCGATAAGTCACTTTATTTGTTTCACTTGTGTCATTTTTATTT 2049
QY 1802 CTCCTTTTGACATTAATCTGTGGCTTTTCTAAATCTTTGTTAAATATATCTATTTTACC 1861
Db 2050 CTCCTTTTGACATTAATCTGTGGCTTTTCTAAATCTTTGTTAAATATATCTATTTTACC 2109
QY 1862 AAAGGTATTTAATATCTTTTTTATGACAACTTAGATCAACTATTTTGTGCTTGTAAAT 1921
Db 2110 AAAGGTATTTAATATCTTTTTTATGACAACTTAGATCAACTATTTTGTGCTTGTAAAT 2169
QY 1922 TTTTCTAAACAAATTTGTATAGCCAGAGGACAAAGATGGATATAAAATATTTGTTGCC 1981

Db 2170 TTTTCTAAACAAATTTGTATAGCCAGAGAAACAAAGATG---ATATAAAATATTTGTTGC 2226
QY 1982 CTGGACAAAATAACATGATATNTCCATCCCGGAATGGTGTAGAGTTGGATTAAACCTGCA 2041
Db 2227 TCTGACAAAATAACATGATATTT---CATTCCTGTATGGTGTAGAGTTAGATT---AATCTGCA 2284
QY 2042 TTTTAAAAAACCTGAATTTGGGAANGAANTTGGTAAGGTTGGCCAAANCTTTTTTTGAAAA 2101
Db 2285 TTTTAAAAAACCTGAATTT---GGATAGATTTGGTAAGTT---GCAAGACCTTTTGGAAAA 2338
QY 2102 TAATTAA 2108
Db 2339 TAATTAA 2345

Search completed: November 26, 2003, 00:11:25
Job time : 398.226 secs

Db 524 CGTTTGATGAAAGATTTGGGCTTGAGACCCAGAGATGACATATGCAAGTATGATTTTG 583
QY 362 TAGAAGTTGAGAACCCAGTGATGGAACCTATATTTAGGGCGCTGGTGGTCTCTGTACTG 421
Db 584 TAGAAGTTGAGAACCCAGTGATGGAACCTATATTTAGGGCGCTGGTGGTCTCTGTACTG 643
QY 422 TACCAGGAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGATCTCGATGAAT 481
Db 644 TACCAGGAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGATCTCGATGAAT 703
QY 482 ATTTTCTCTGTAACCCAGGTTCTGCACTCACTACACATTTGTCATGCCACAATTCACAG 541
Db 704 ATTTTCTCTGTAACCCAGGTTCTGCACTCACTACACATTTGTCATGCCACAATTCACAG 763
QY 542 AAGCTGTGAGTCCTTCAGTGCTACCCCTTTCAGCTTTGCCACTGGACCTCTTAATAAG 601
Db 764 AAGCTGTGAGTCCTTCAGTGCTACCCCTTTCAGCTTTGCCACTGGACCTCTTAATAAG 823
QY 602 CTATAACCTGTTTGTACCTTTGGAAGACCTTATTCGATATCTTGAACGAGAGATGGC 661
Db 824 CTATAACCTGTTTGTACCTTTGGAAGACCTTATTCGATATCTTGAACGAGAGATGGC 883
QY 662 AGTTGGACTTAGAAGACTCTATATAGGCCAACTTGGCAAGCTTTTGGTCTTTT 721
Db 884 AGTTGGACTTAGAAGACTCTATATAGGCCAACTTGGCAAGCTTTTGGTCTTTT 943
QY 722 TTGGAGAAATCCAGAGTGTGATCTGACCTTCTAAGAGAGAGGTAAAGTATATACA 781
Db 944 TTGGAGAAATCCAGAGTGTGATCTGACCTTCTAAGAGAGAGGTAAAGTATATACA 1003
QY 782 GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCA 841
Db 1004 GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCA 1063
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Db 1184 TTCAGTTGAGACCAAGAACCCGTTGTCAGGGAATTCACAAATCTCACCGACGTGGCCC 1243
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QY 1082 ACCACCAAGCTCTTGCCCAAGAGTGTGCAAGTGTGCTGATTTCTATTAGAGAACGT 1141
Db 1304 ACCACCAAGCTCTTGCCCAAGAGTGTGCAAGTGTGCTGATTTCTATTAGAGAACGT 1363
QY 1142 ATGGGTATCTCCATCTTATCTCAGTGTGTTGCTTCAAGGACCTTTCATCTCAGAT 1201
Db 1364 ATGGGTATCTCCATCTTATCTCAGTGTGTTGCTTCAAGGACCTTTCATCTCAGAT 1423
QY 1202 TTACAGTGCATTTCTGAAAGAGGAGACATCAACAGAAATAGGAGTTGTGCAACAGCTCTT 1261
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QY 1262 TTGAGAGAGGCTTAAAGACAGGAGAAAGGTCTTCAATCGTGAAGAAATTAATG 1321
Db 1484 TTGAGAGAGGCTTAAAGACAGGAGAAAGGTCTTCAATCGTGAAGAAATTAATG 1543
QY 1322 TTGATTAATTAAGATCACAGCTAGTTTTCAGAGTTTACCATGTATCTTCCACTAGCTGG 1381
Db 1544 TTGATTAATTAAGATCACAGCTAGTTTTCAGAGTTTACCATGTATCTTCCACTAGCTGG 1603
QY 1382 GTTCTGTATTTTCAGTCTTTTCGATACCGCTTAGGGAATGTCAGTACAGGAAAAAATG 1441

Db 1604 GTTCTGTATTTTCAGTTCTTTTCGATACGCTTAGGGTAATGTCAGTACAGGAAAAAACTG 1663
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Db 1664 TGCAAGTGAGCACCTGATTCGCTTTCGCTTAACTCTAAAGCTCCATGTCCTGGGCT 1723
QY 1502 AAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGTAAC 1561
Db 1724 AAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGTAAC 1783
QY 1562 AGAATCTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATPAA 1621
Db 1784 AGAATCTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATPAA 1843
QY 1622 ACTGTGTCCTGCTGATAGGACAGCTGGATTTTTTCTATTTCTTATTTAAAAATTTCTGCC 1681
Db 1844 ACTGTGTCCTGCTGATAGGACAGCTGGATTTTTTCTATTTCTTATTTAAAAATTTCTGCC 1903
QY 1682 ATTTAGAGAGAGAACTACATTTCTGTTTGGAGAGATAAACTGAAAAAGAGAGTGG 1741
Db 1904 ATTTAGAGAGAGAACTACATTTCTGTTTGGAGAGATAAACTGAAAAAGAGAGTGG 1963
QY 1742 CCTATCTCTACCTTATCGATAAGTCAGTTTATTTGTTTCAATGTGTGACATTTTATAT 1801
Db 1964 CCTATCTCTACCTTATCGATAAGTCAGTTTATTTGTTTCAATGTGTGACATTTTATAT 2023
QY 1802 CTCCTTTTGACATTAATACTGTTGGCTTTTCTAACTCTGTTAAATATATCTATTTTACC 1861
Db 2024 CTCCTTTTGACATTAATACTGTTGGCTTTTCTAACTCTGTTAAATATATCTATTTTACC 2083
QY 1862 AAAGGTATTTAATTTCTTTTATGACAACTTAGATCAACTATTTTCTAGCTTGTGTAAT 1921
Db 2084 AAAGGTATTTAATTTCTTTTATGACAACTTAGATCAACTATTTTCTAGCTTGTGTAAT 2143
QY 1922 TTTTCTAAACAAATGTTTATAGCCAGAGGACAAAGATG---ATATAAATATTGTTGCC 1981
Db 2144 TTTTCTAAACAAATGTTTATAGCCAGAGGACAAAGATG---ATATAAATATTGTTGCC 2200
QY 1982 CTGGCAAAAAATACATGTATNTCCATCCGGAATGCTGAGAGTTGGATTAAACCTGCA 2041
Db 2201 TCTGACAAAAATACATGTATTT---CATTTCTGATGCTGATAGATT---AATCTGCA 2258
QY 2042 TTTTAAAAAACCTGATTTGGGAAGGAATTTGGTAAGTTGGCCAAANCTTTTTTGA 2101
Db 2259 TTTTAAAAAACCTGATTT---GGAATAGAAATGGTAAGTT---GCAAGACCTTTTTTGA 2312
QY 2102 TAAATTA 2108
Db 2313 TAAATTA 2319

RESULT 2

US-09-265-686-1
; Sequence 1, Application US/09265686
; Patent No. 6455283
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
; FILE REFERENCE: P1122P2
; CURRENT APPLICATION NUMBER: US/09/265,686
; CURRENT FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: US 09/040,220
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: US 09/184,216
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 1
; LENGTH: 2825
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: Unknown

; LOCATION: 2689									
; OTHER INFORMATION: Any nucleotide									
US-09-265-686-1									
Query Match 93.9%; Score 1979.4; DB 4; Length 2825;									
Best Local Similarity 97.7%; Pred. No. 0;									
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;									
QY	2	CCGCGCGTGTAGTACCTCTCAACCCAGTACGCAAAATGAGCCCTTCGCGCTCTCTCTGG	61						
DB	224	CCGCGCGTGTAGTACCTCTCAACCCAGTACGCAAAATGAGCCCTTCGCGCTCTCTCTGG	283						
QY	62	TGACATCTGCCCTGCGCGCGAGAGACGAGGAGCTCAGCGGATCCAACTCGAGTAGTA	121						
DB	284	TGACATCTGCCCTGCGCGCGAGAGACGAGGAGCTCAGCGGATCCAACTCGAGTAGTA	343						
QY	122	AATTCAGTCTTCCAGCAACAGGAAACAGACGAGTACAAGTCTTCAGCATGAGAGAA	181						
DB	344	AATTCAGTCTTCCAGCAACAGGAAACAGACGAGTACAAGTCTTCAGCATGAGAGAA	403						
QY	182	TTATTACTGTCTACTAATGGAAGTATTCAGCCCAAGGTTCTCTACTATTCCTCA	241						
DB	404	TTATTACTGTCTACTAATGGAAGTATTCAGCCCAAGGTTCTCTACTATTCCTCA	463						
QY	242	GAAATACGGTCTTGGTATGAGATTTAGTAGCAGTAGAGGAAATGTATGATACAACCTTA	301						
DB	464	GAAATACGGTCTTGGTATGAGATTTAGTAGCAGTAGAGGAAATGTATGATACAACCTTA	523						
QY	302	CGTTTGATGAAAGATTTGGGCTTGAGACCCAGAGATGACATATGCAAGTATGATTTG	361						
DB	524	CGTTTGATGAAAGATTTGGGCTTGAGACCCAGAGATGACATATGCAAGTATGATTTG	583						
QY	362	TAGAAAGTTGAGGAAACCCAGTATGATGAACTATATTAGGGCGCTGCTGCTCTGGTACTG	421						
DB	584	TAGAAAGTTGAGGAAACCCAGTATGATGAACTATATTAGGGCGCTGCTGCTCTGGTACTG	643						
QY	422	TACAGGAAACAGATTTCTAAAGGAATCAAAATAGAGTAAGATTTGTATCTGATGAAT	481						
DB	644	TACAGGAAACAGATTTCTAAAGGAATCAAAATAGAGTAAGATTTGTATCTGATGAAT	703						
QY	482	ATTTTCTCTTCAACACGAGGTTCTGCATCCACTCAACATTTGCATGCCACAATTCACAG	541						
DB	704	ATTTTCTCTTCAACACGAGGTTCTGCATCCACTCAACATTTGCATGCCACAATTCACAG	763						
QY	542	AGCTGTGAGTCTCTTCACTGCTACCCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTT	601						
DB	764	AGCTGTGAGTCTCTTCACTGCTACCCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTT	823						
QY	602	CTATAACTGCTCTTCTAGTACCTTGGAGACCTTATTCGATATCTTGAACAGAGAGATGGC	661						
DB	824	CTATAACTGCTCTTCTAGTACCTTGGAGACCTTATTCGATATCTTGAACAGAGAGATGGC	883						
QY	662	AGTTGAGCTTGAAGATCTATATAGGCAACTTGGCAACTTCTTGGCAAGGCTTTTGT	721						
DB	884	AGTTGAGCTTGAAGATCTATATAGGCAACTTGGCAACTTCTTGGCAAGGCTTTTGT	943						
QY	722	TTGGAGAGAAATCCAGAGTGTGGATCTGAACCTTCTAAACAGAGAGTATATACA	781						
DB	944	TTGGAGAGAAATCCAGAGTGTGGATCTGAACCTTCTAAACAGAGAGTATATACA	1003						
QY	782	GCTGCACACTCGTAACTTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACCGATACCA	841						
DB	1004	GCTGCACACTCGTAACTTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACCGATACCA	1063						
QY	842	TTTTCTGGCCAGTGTCTCTGTTTAAACGCTGTGGGAACTGTGCTGTTGCTCC	901						
DB	1064	TTTTCTGGCCAGTGTCTCTGTTTAAACGCTGTGGGAACTGTGCTGTTGCTCC	1123						
QY	902	ACAAATGCAATGAATGTCAATGTGCTCCCAAGCAAAAGTTACTAAATAATACCAAGGTCC	961						
DB	1124	ACAAATGCAATGAATGTCAATGTGCTCCCAAGCAAAAGTTACTAAATAATACCAAGGTCC	1183						
QY	962	TTCAAGTTGAGACCAAGACCGGTGTACGGGATTCGACAAATCTACCCAGCTGGGCC	1021						

DB	1184	TTCAAGTTGAGACCAAGACCGGTGTACGGGATTCGACAAATCACTACCCAGCTGGGCC	1243						
QY	1022	TGGAGACCAATGAGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGTAGCCGATC	1081						
DB	1244	TGGAGACCAATGAGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGTAGCCGATC	1303						
QY	1082	ACCACAGAGCTCTTGGCCAGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG	1141						
DB	1304	ACCACAGAGCTCTTGGCCAGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG	1363						
QY	1142	ATGCGTGTATCTCATCTTAAATCTCAGTGTGTTTGTCTCAAGGACCTTTCATCTTCAGGAT	1201						
DB	1364	ATGCGTGTATCTCATCTTAAATCTCAGTGTGTTTGTCTCAAGGACCTTTCATCTTCAGGAT	1423						
QY	1202	TTACAGTGTATCTGAAAGAGAGACATCAAAACAGATTTAGAGTGTGCAACAGCTCTT	1261						
DB	1424	TTACAGTGTATCTGAAAGAGAGACATCAAAACAGATTTAGAGTGTGCAACAGCTCTT	1483						
QY	1262	TTGAGAGGAGGCTTAAAGCAGAGGAGAAAGTCTTCAATCGTGAAGAAATTAATG	1321						
DB	1484	TTGAGAGGAGGCTTAAAGCAGAGGAGAAAGTCTTCAATCGTGAAGAAATTAATG	1543						
QY	1322	TTGTATTAATAGATCACAGCTAGTTTCAGAGTTCACATGTACGTATTCACATGTG	1381						
DB	1544	TTGTATTAATAGATCACAGCTAGTTTCAGAGTTCACATGTACGTATTCACATGTG	1603						
QY	1382	GTTCTGTATTTTCAGTCTTTCGATACGGCTTAGGGTAATGTGATGACAGGAAATAA	1441						
DB	1604	GTTCTGTATTTTCAGTCTTTCGATACGGCTTAGGGTAATGTGATGACAGGAAATAA	1663						
QY	1442	TGCAAGTGTAGACCTGATTCGGTTCGCTTAACTCTAAAGCTTCAATGTCTGGGCT	1501						
DB	1664	TGCAAGTGTAGACCTGATTCGGTTCGCTTAACTCTAAAGCTTCAATGTCTGGGCT	1723						
QY	1502	AAATTCGTATTAATCTGGATTTTCTGCTTCTGCTCATATTCATATTCATATTC	1561						
DB	1724	AAATTCGTATTAATCTGGATTTTCTGCTTCTGCTCATATTCATATTCATATTC	1783						
QY	1562	AGAACATTTCTATGTACTCAAACTGGTCTTAAAGGAACTATGTTGCTATGAATTA	1621						
DB	1784	AGAACATTTCTATGTACTCAAACTGGTCTTAAAGGAACTATGTTGCTATGAATTA	1843						
QY	1622	ACTGTGCTGCTGCTGATAGGACAGACTGATTTTCTATTTCTATTTAAATTTCTGC	1681						
DB	1844	ACTGTGCTGCTGCTGATAGGACAGACTGATTTTCTATTTCTATTTAAATTTCTGC	1903						
QY	1682	ATTTAGAGAGAGAACTACATTCATGTTTGGAGAGATAAACTGAAAGAGAGTGG	1741						
DB	1904	ATTTAGAGAGAGAACTACATTCATGTTTGGAGAGATAAACTGAAAGAGAGTGG	1963						
QY	1742	CTTTATCTTCACTTTATCGATTAAGTCAATTTTGTGTTTCAATTTGTTATTTAT	1801						
DB	1964	CTTTATCTTCACTTTATCGATTAAGTCAATTTTGTGTTTCAATTTGTTATTTAT	2023						
QY	1802	CTCTTTTTCACATTAATCTGTTGCTTTCTTAATCTTGTAAATATATCTATTTTACC	1861						
DB	2024	CTCTTTTTCACATTAATCTGTTGCTTTCTTAATCTTGTAAATATATCTATTTTACC	2083						
QY	1862	AAAGGTATTTAAATATCTTTTATATGACAACTTAGATCAACTATTTTGTGCTTAAAT	1921						
DB	2084	AAAGGTATTTAAATATCTTTTATATGACAACTTAGATCAACTATTTTGTGCTTAAAT	2143						
QY	1922	TTTTCTTAAACAAATTTATAGCCAGAGGACAAAGATGATAAAATATTTGTTGCC	1981						
DB	2144	TTTTCTTAAACAAATTTATAGCCAGAGGACAAAGATGATAAAATATTTGTTGCC	2200						
QY	1982	CTGGACAAATAATACATGTATNTCCATCCCGGAATGGTGTAGAGTTGATTAACCTGCA	2041						
DB	2201	CTGGACAAATAATACATGTATNTCCATCCCGGAATGGTGTAGAGTTGATTAACCTGCA	2258						
QY	2042	TTTTTAAATAACCTGAAATTTGGGAAGGAATTTGGTAAAGCTTTTGTGCTTGTGAAA	2101						

Db 2259 TTTTAAAAAAGTGAATT---GGAATAGAAATTGGTAAGTT---GCAAGAGACTTTTGAAAA 2312

Qy 2102 TAAATTA 2108

Db 2313 TAAATTA 2319

RESULT 3

US-09-564-595D-32
; Sequence 32, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-09-564-595D-32

Query Match 77.1%; Score 1624.8; DB 4; Length 1760;
Best local similarity 99.7%; Pred. No. 0;
Matches 1637; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 2 CCCGCCGTGAGTGAAGTCTCACCCAGTCAGCCAAATCAGAGCTCTTCGGGCTTCCTCGG 61
Db 119 CCCGCCGTGAGTGAAGTCTCACCCAGTCAGCCAAATCAGAGCTCTTCGGGCTTCCTCG 178
Qy 62 TGACATCTGCTCCGCGCGCAGAGACGAGGAGCTCAGCGCGAATCCAACTGAGTAGTA 121
Db 179 TGACATCTGCTCCGCGCGCAGAGACGAGGAGCTCAGCGCGAATCCAACTGAGTAGTA 238
Qy 122 AATTCAGTCTTCCAGCAACAGGAAACAGACGAGTACAGATCCTCAGCATGAGAGAA 181
Db 239 AATTCAGTCTTCCAGCAACAGGAAACAGACGAGTACAGATCCTCAGCATGAGAGAA 298
Qy 182 TTAATACGTCTCTAATAGAAATTAATCAGCCCAAGGTTTCCTCATCTATCCAA 241
Db 299 TTAATACGTCTCTAATAGAAATTAATCAGCCCAAGGTTTCCTCATCTATCCAA 358
Qy 242 GAAATACGTCTTGGTATGAGATAGTAGAGTACAGGAAATGATGATGATGATGATGAT 301
Db 359 GAAATACGTCTTGGTATGAGATAGTAGAGTACAGGAAATGATGATGATGATGATGAT 418
Qy 302 CGTTGATGAAAGATTTGGGCTTGAAGCCCAAGAGATGACATATGCAAGTATGATTTG 361
Db 419 CGTTGATGAAAGATTTGGGCTTGAAGCCCAAGAGATGACATATGCAAGTATGATTTG 478
Qy 362 TAGAAGTCTAGGAAACCCAGTGTGAACTATATATAGGCGCTGGTGTGTTCTGGTACTG 421
Db 479 TAGAAGTCTAGGAAACCCAGTGTGAACTATATATAGGCGCTGGTGTGTTCTGGTACTG 538
Qy 422 TACCAGGAAAAACAGATTTCTTAAGGAAATCAAAATAGGATAGATTTCTATCTGATGAAT 481
Db 539 TACCAGGAAAAACAGATTTCTTAAGGAAATCAAAATAGGATAGATTTCTATCTGATGAAT 598
Qy 482 ATTTCTCTCTGAAACAGGAGTCTGATCCACTCAACATTTGTCATGCAACAAATTCAG 541

Db 599 ATTTTCTCTTGAACAGGGTCTGCATCCACTCAACATTTGTATGCCAAATTCACAG 658
Qy 542 AAGCTGTGAGTCCCTTCACTGCTACCCCTTCCAGCTTTGCCACTGAGCTCTTAATAATG 601
Db 659 AAGCTGTGAGTCCCTTCACTGCTACCCCTTCCAGCTTTGCCACTGAGCTCTTAATAATG 718
Qy 602 CTATAACTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACAGAGAGATGCC 661
Db 719 CTATAACTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACAGAGAGATGCC 778
Qy 662 AGTTGCACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTTGGCAAGGCTTTTGT 721
Db 779 AGTTGCACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTTGGCAAGGCTTTTGT 838
Qy 722 TTGGAAGAAATCCAGAGTGTGATCGAACCTTTAAACAGAGAGAGTATATACA 781
Db 839 TTGGAAGAAATCCAGAGTGTGATCGAACCTTTAAACAGAGAGAGTATATACA 898
Qy 782 GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGAGAACTAAAGAGAACCCATACCA 841
Db 899 GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGAGAACTAAAGAGAACCCATACCA 958
Qy 842 TTTTCTGCGCAGGTTGTCTCTGTTTAAACGCTGTGTGGGAACTGTGCTGTCTCTCC 901
Db 959 TTTTCTGCGCAGGTTGTCTCTGTTTAAACGCTGTGTGGGAACTGTGCTGTCTCTCC 1018
Qy 902 ACAATTGCATGAATGTCAATGTCTCCCAAGCAAGTTACTTAAATAATACCACAGGCTCC 961
Db 1019 ACAATTGCATGAATGTCAATGTCTCCCAAGCAAGTTACTTAAATAATACCACAGGCTCC 1078
Qy 962 TTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTCACAAATCTACTCACCGCTGGGCC 1021
Db 1079 TTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTCACAAATCTACTCACCGCTGGGCC 1138
Qy 1022 TGAGACCATCAGAGTGTGATCTGTGTGAGAGGGAGCACAGGAGATAGCGGATC 1081
Db 1139 TGAGACCATCAGAGTGTGATCTGTGTGAGAGGGAGCACAGGAGATAGCGGATC 1198
Qy 1082 ACCACAGCAGCTCTTGTCCAGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1141
Db 1199 ACCACAGCAGCTCTTGTCCAGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1258
Qy 1142 ATGCGTTATCTCATCTTAACTCTCAGTGTGTGCTTCAAGGACCTTTCATCTTCAGGAT 1201
Db 1259 ATGCGTTATCTCATCTTAACTCTCAGTGTGTGCTTCAAGGACCTTTCATCTTCAGGAT 1318
Qy 1202 TTACAGTGTCAATCTGAAAGAGAGACATCAACAGAAATTAGGAGTTGTGCAACAGCTCT 1261
Db 1319 TTACAGTGTCAATCTGAAAGAGAGACATCAACAGAAATTAGGAGTTGTGCAACAGCTCT 1378
Qy 1262 TTGAGAGAGGCTTAAAGACAGGAGAAAGTCTTCAATCTGTGAAAGAAATTAATG 1321
Db 1379 TTGAGAGAGGCTTAAAGACAGGAGAAAGTCTTCAATCTGTGAAAGAAATTAATG 1438
Qy 1322 TTGATTTAAATAGATCACCAGCTAGTTTCAGAGTTTACCATGTACGTATTCACCTAGCTGG 1381
Db 1439 TTGATTTAAATAGATCACCAGCTAGTTTCAGAGTTTACCATGTACGTATTCACCTAGCTGG 1498
Qy 1382 GTTCTGATTTTCACTTCTTTCGATACGGCTTAGGGTAAATGTGATGAGGAGGAGGAGGAG 1441
Db 1499 GTTCTGATTTTCACTTCTTTCGATACGGCTTAGGGTAAATGTGATGAGGAGGAGGAGGAG 1558
Qy 1442 TCCAGTGTAGCAGCTGTGATTCGCTTGTCTTAACTCTTAAAGCTCCATGTCTCTGGGCT 1501
Db 1559 TCCAGTGTAGCAGCTGTGATTCGCTTGTCTTAACTCTTAAAGCTCCATGTCTCTGGGCT 1618
Qy 1502 AAAATCGTATAAAATCTGGA-TTTTTTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGTAAC 1560
Db 1619 AAAATCGTATAAAATCTGGA-TTTTTTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGTAAC 1678
Qy 1561 CAGAACATTTCTATGTAACAACCTGGTTTTTAAAGAGGAACTATGTGCTATGAATTA 1620

Db 1679 CAGAACATTTCTATGCTACAAACCTGGTTTTTAAAGAGAACTATGTTGCTATGAATTA 1738
Qy 1621 AACTTGTGTCRTGCTGATAGGA 1642
Db 1739 AACTTGTGCTGCTGATAGGA 1760

RESULT 4
US-09-706-968-1
; Sequence 1, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVGF3
; FILE REFERENCE: 98-60CI
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-09-706-968-1

Query Match 77.1%; Score 1624.8; DB 4; Length 1760;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1637; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 2 CCCGCGGTGAGTGAGCTCTCACCCAGTCAGCAAAATGAGCTCTTCGGGCTTCCTCGG 61
Db 119 CCCGCGGTGAGTGAGCTCTCACCCAGTCAGCAAAATGAGCTCTTCGGGCTTCCTCG 178
Qy 62 TGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 121
Db 179 TGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 238
Qy 122 RAATCCAGTTTCCAGCAACAGGAAACAGAACCGAGTACAGATCCTCAGCATGAGAGAA 181
Db 239 RAATCCAGTTTCCAGCAACAGGAAACAGAACCGAGTACAGATCCTCAGCATGAGAGAA 298
Qy 182 TTATTAATGCTGCTACTAATGGAAGTATTCAGCCCAAGGTTTCCCTCATCTATCCAA 241
Db 299 TTATTAATGCTGCTACTAATGGAAGTATTCAGCCCAAGGTTTCCCTCATCTATCCAA 358
Qy 242 GAAATACGCTCTTGCTATGAGATTTAGTAGCAGTAGAGGAAAATGATGATGATCACTTA 301
Db 359 GAAATACGCTCTTGCTATGAGATTTAGTAGCAGTAGAGGAAAATGATGATGATCACTTA 418
Qy 302 CTTTTGATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGATGATGATTTG 361
Db 419 CTTTTGATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGATGATGATTTG 478
Qy 362 TAGAAGTTGAGAAACCCAGTGTATGAACTATATATAGGCGCTGCTGCTGCTGCTGCTG 421
Db 479 TAGAAGTTGAGAAACCCAGTGTATGAACTATATATAGGCGCTGCTGCTGCTGCTGCTG 538
Qy 422 TACCAGGAAAACAGATTTCTTAAGGAAATCAAAATAGGATTAAGATTTGTTATCTGATGA 481
Db 539 TACCAGGAAAACAGATTTCTTAAGGAAATCAAAATAGGATTAAGATTTGTTATCTGATGA 598
Qy 482 AITTTTCTTCTGAAACCGGTTCTGCAATCCACTACAACTTGTCTATGCCCAATTCACAG 541

Db 599 APTTTCCTTCTGAAACAGGGTTCGATCCCAACATTTGCTATGCCCAATTCACAG 658
Qy 542 AAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGCGCACTGCACTGCTTAATAATG 601
Db 659 AAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTGCGCACTGCACTGCTTAATAATG 718
Qy 602 CTATTAATCTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCAAGAGATGTC 661
Db 719 CTATAAATCTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCAAGAGATGTC 778
Qy 662 AGTTGCACTTAGAAGATCTATATAGGCACTTTCGCAACTTCTTGGCAAGGCTTTTGT 721
Db 779 AGTTGCACTTAGAAGATCTATATAGGCACTTTCGCAACTTCTTGGCAAGGCTTTTGT 838
Qy 722 TTGGAAGAAAATCCAGAGTGTGATCTGAACCTTCTTAACAGAGAGGTATGATATACA 781
Db 839 TTGGAAGAAAATCCAGAGTGTGATCTGAACCTTCTTAACAGAGAGGTATGATATACA 898
Qy 782 GCTGCACACCTCGTAACCTTCTCAGTGTCTCAAGGGAAGAACTAAAGAAACCGATACCA 841
Db 899 GCTGCACACCTCGTAACCTTCTCAGTGTCTCAAGGGAAGAACTAAAGAAACCGATACCA 958
Qy 842 TTTTCTGCGCCAGGTTGTCTCTGCTTAAACGCTGTGTGGGAACCTGCTGCTTGTCTCC 901
Db 959 TTTTCTGCGCCAGGTTGTCTCTGCTTAAACGCTGTGTGGGAACCTGCTGCTTGTCTCC 1018
Qy 902 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAGTTTACTAAAAATACCAACAGGTC 961
Db 1019 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAGTTTACTAAAAATACCAACAGGTC 1078
Qy 962 TTCAGTTGAGACCAAGACCGGTGTCAAGGGAATGCAAAATCACTACCAACGTCGCGCC 1021
Db 1079 TTCAGTTGAGACCAAGACCGGTGTCAAGGGAATGCAAAATCACTACCAACGTCGCGCC 1138
Qy 1022 TGGAGCACTGAGAGTGTGACTGTGTGTCGAGGAGGACACAGGAGTAGCGGATC 1081
Db 1139 TGGAGCACTGAGAGTGTGACTGTGTGTCGAGGAGGACACAGGAGTAGCGGATC 1198
Qy 1082 ACCACAGCAGCTCTTGGCCAGAGCTGTGCAAGTGTGCTGCTGATTTCTATTAGAGAACGT 1141
Db 1199 ACCACAGCAGCTCTTGGCCAGAGCTGTGCAAGTGTGCTGCTGATTTCTATTAGAGAACGT 1258
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Db 1259 ATGCGTTATCTCATCTTAATCTCAGTGTGTTGCTTCAAGACCTTTCATCTTCAGGAT 1318
Qy 1202 TTACAGTGTGATTTCTGAAAGAGAGACATCAAAACAGATTTAGGAGTTGTGCAACAGCTCT 1261
Db 1319 TTACAGTGTGATTTCTGAAAGAGAGACATCAAAACAGATTTAGGAGTTGTGCAACAGCTCT 1378
Qy 1262 TTGAGAGGAGGCTTAAAGACAGGAGAAAAGGTCTTCAATCTGTGAAAGAAAATTAATG 1321
Db 1379 TTGAGAGGAGGCTTAAAGACAGGAGAAAAGGTCTTCAATCTGTGAAAGAAAATTAATG 1438
Qy 1322 TTGTTATTAATAGATCACCACTGTTTTCAGAGTTTACCATGTACCTATTTCCACTAGCTGG 1381
Db 1439 TTGTTATTAATAGATCACCACTGTTTTCAGAGTTTACCATGTACCTATTTCCACTAGCTGG 1498
Qy 1382 GTTCTGTATTTTCAGTTCCTTTCGATACGCTTGTAGGTAATGTGATGAGGAAAACCTG 1441
Db 1499 GTTCTGTATTTTCAGTTCCTTTCGATACGCTTGTAGGTAATGTGATGAGGAAAACCTG 1558
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Db 1559 TCGAAGTGTGAGGAGGCTTTCGCTGCTTGTCTTCACTTCAAGCTTCAATGCTTGGGCT 1618
Qy 1502 AAAATCGTATAAAATCTGGA-TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1560
Db 1619 AAAATCGTATAAAATCTGGA-TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1678
Qy 1561 CAGACATCTATGTACTACAAACCTGTTTAAAGAGGAACTATGTGTCTATGAATTA 1620

1679 CAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGAATTA 1738

1621 AACTTGTCRTGCTGATAGGA 1642
Ov

Db 1739 AACTTGTGTCGTGCTAGGA 1760

RESULT 5

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US-09-457-066-1
; Sequence 1, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154) ... (1191)
US-09-457-066-1

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Query Match 76.4%; Score 1610.8; DB 4; Length 1764;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1637; Conservative 1; Mismatches 3; Indels 5; Gaps 2;

Qy	2	CCGCGCGTGAGTACTCTCACCCACGCTCAGCCAAATGAGCCTCTCTGGGCTTCTCCTCGG	61
Db	119	CCGCGCGTGAGTACTCTCACCCACGCTCAGCCAAATGAGCCTCTCTGGGCTTCTCCTCGC	178
Qy	62	TGACATCTGCGCTGGCGCGGCAGAGACGAGGGACTCAGCGGGAAATCCAACTCGAGTAGTA	121
Db	179	TGACATCTGCGCTGGCGCGGCAGAGACGAGGGACTCAGCGGGAAATCCAACTCGAGTAGTA	238
Qy	122	AAATTCACAGTTTTTCAGCAACAAGGAAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAA	181
Db	239	AAATTCACAGTTTTTCAGCAACAAGGAAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAA	298
Qy	182	TTATTAATCTGTCGTACTACTAATCGGAGTAGTATTCACAGCCCAAGGTTTCTCTATACTTATCCAA	241
Db	299	TTATTAATCTGTCGTACTACTAATCGGAGTAGTATTCACAGCCCAAGGTTTCTCTATACTTATCCAA	358
Qy	242	GAAATAACGCTCTTGATATGGAGATTTAGTAGCAGTAGAGGAAATGATATCGATACAACTTA	301
Db	359	GAAATAACGCTCTTGATATGGAGATTTAGTAGCAGTAGAGGAAATGATATCGATACAACTTA	418
Qy	302	CGTTTGATCAAGATTTTCGGCTTCAGACCCAGAGATGACATATCGAGTAGTATGTTTG	361
Db	419	CGTTTGATCAAGATTTTCGGCTTCAGACCCAGAGATGACATATCGAGTAGTATGTTTG	478
Qy	362	TAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTTCTGTAATCTG	421
Db	479	TAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTTCTGTAATCTG	538
Qy	422	TACCGGGAACACAGATTTCTTAAGGGAATCAAAATTGGAATAGATTTGATCTGATGAAT	481
Db	539	TACCGGGAACACAGATTTCTTAAGGGAATCAAAATTGGAATAGATTTGATCTGATGAAT	598
Qy	482	ATTTTCCTTCTGAACACGAGGTTCTGCATCCACTACAACTTGTCATGCCCAAAATTCACAG	541
Db	599	ATTTTCCTTCTGAACACGAGGTTCTGCATCCACTACAACTTGTCATGCCCAAAATTCACAG	658

200 CTAATGGAAGTAATTCACAGCCCAAGGTTTCTCTCATACTTATCCAGAAATACGGTCTTGG 259
257 TATGGAGATTAGTAGCAGTAGAGGAAATCTATGGATACAACTTACGTTTGTATGAAGAT 316
260 TATGGAGATTAGTAGCAGTAGAGGAAATCTATGGATACAACTTACGTTTGTATGAAGAT 319
317 TTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTGTAGAGTTGAGGAAC 376
320 TTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTGTAGAGTTGAGGAAC 379
377 CCAGTGATGAACTATATATAGGCGCTGGTGTCTGTACTGTACCTGACAGGAAACAGA 436
380 CCAGTGATGAACTATATATAGGCGCTGGTGTCTGTACTGTACCTGACAGGAAACAGA 439
437 TTTCTAAGGAAATCAATATAGGATAGATTTGTATCTGTATGATGAATATTTCTTCTGAAC 496
440 TTTCTAAGGAAATCAATATAGGATAGATTTGTATCTGTATGATGAATATTTCTTCTGAAC 499
497 CAGGTTCTGCATCCATCAACATTTGATGATGATGATGATGATGATGATGATGATGATG 556
500 CAGGTTCTGCATCCATCAACATTTGATGATGATGATGATGATGATGATGATGATGATG 559
557 CAGTGTACCCCTTCACTGCTTTGCCATGCACTGCTGCTTAAATATGCTATACTGCTTAA 616
560 CAGTGTACCCCTTCACTGCTTTGCCATGCACTGCTGCTTAAATATGCTATACTGCTTAA 619
617 GTACCTTGGAGACCTTATTCGATATCTTGAACCCAGAGATGCGAGTTGGACTTAGAAG 676
620 GTACCTTGGAGACCTTATTCGATATCTTGAACCCAGAGATGCGAGTTGGACTTAGAAG 679
677 ATCTATATAGCCCACTTGGCACTTCTTGGCAAGGCTTTTGTGTTTGGAGAAATCCA 736
680 ATCTATATAGCCCACTTGGCACTTCTTGGCAAGGCTTTTGTGTTTGGAGAAATCCA 739
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740 GAGTGTGGATCTGAACTTCTTACAGAGAGGTAGATATACAGTGTGCACTCGTA 799
797 ACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGCCAGGTT 856
800 ACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGCCAGGTT 859
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860 GTCTCTGTTTAAACGCTGTGGGAACTGTGCTGTTGCTCTCCAAATTCGAATGAAT 919
917 GTCAATGTGCCAAGCAAAAGTTACTTAAATAATACCAAGAGTCTTTCAGTTGAGACCAA 976
920 GTCAATGTGCCAAGCAAAAGTTACTTAAATAATACCAAGAGTCTTTCAGTTGAGACCAA 979
977 AGACCGGTGTCCAGGGATTCACAAATCACTCACCGAGTGGCCCTGGAGCACCATGAGG 1036
980 AGACCGGTGTCCAGGGATTCACAAATCACTCACCGAGTGGCCCTGGAGCACCATGAGG 1039
1037 AGTGTGACTGTGTGACAGGGGAGCAGGAGGATAG 1074
1040 AGTGTGACTGTGTGACAGGGGAGCAGGAGGATAG 1077

RESULT 8

US-09-564-595D-34
; Sequence 34, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03

; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 3571
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1049)...(2086)
US-09-564-595D-34

Query Match 45.5%; Score 959.4; DB 4; Length 3571;
Best Local Similarity 70.3%; Pred. No. 6.4e-235;
Matches 1446; Conservative 1; Mismatches 578; Indels 31; Gaps 11;
Qy 2 CCGCCCTGAGTGAGCTCTCACCCAGTCAGCCCAATGAGCCCTTTCGGGCTTCTCTCG 61
Db 1014 CCGCCCGGAGTAGGCTCTCGCCCGAGTCAGCCCAATGAGCCCTTTCGGGCTTCTCTCG 1073
Qy 62 TGACATCTGCTGCTGCGCGCCAGAGACGAGGAGTCTCAGCGGAAATCCAACTGAGTGA 121
Db 1074 TGACATCTGCTGCTGCGCGCCAAAGAACGCGGAGTCTGCGGCTGAGTCCAACTGAGCAGCA 1133
Qy 122 AATTCAGTCTTCAGCAACAAGGACAGACGAGGTACAGATCTCAGCATGAGAGAA 181
Db 1134 AGTTGCACTCTCAGCGCAGCAAGGACAGACGAGGTGCAAGATCCCCGCGCATGAGAGAG 1193
Qy 182 TTATTACTGTCTTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATACTTATCCAA 241
Db 1194 TTGTCACTATCTGTTAATGGGAGCATCCACAGCCCGAAGTTTCTCATACATACCCA 1253
Qy 242 GAAATACGCTCTTGATGATGAGATAGTAGCAGTAGAGGAAATATGATGATGATGATGAT 301
Db 1254 GAAATATGCTGCTGCTGCTGAGATAGTTGTCAGTAGTAAATGTCGCGATCCAGCTGA 1313
Qy 302 CGTTTGTATGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTG 361
Db 1314 CATTTGATGAGATTTGGGCTGGAAGATCCAGAGACGATATATGCAAGTATGATTTTG 1373
Qy 362 TAGAAGTTGAGAACCCAGGATGAGTATGATGAGGCGCTGCTGCTGCTGCTGCTGCTGCTG 421
Db 1374 TAGAAGTTGAGAACCCAGGATGAGTATGATGAGGCGCTGCTGCTGCTGCTGCTGCTGCTG 1433
Qy 422 TACCAGGAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTTGATCTGATGAAT 481
Db 1434 TGCCAGGAAACAGATTTCTAAAGGAAATCAATATCAGGATAAGATTTGATCTGATGAT 1493
Qy 482 ATTTTCTTCTGAACCGGTTCTGATCCACTACACATTTGATGATGATGATGATGATGATGAT 541
Db 1494 ATTTTCTTCTGAACCGGTTCTGATCCACTACACATTTGATGATGATGATGATGATGATGAT 1553
Qy 542 AAGCTGTGAGTCTTCACTGCTACCCCTTCACTGCTTGGCCACTGAGCTCTTAAATG 601
Db 1554 AAAACAAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1613
Qy 602 CTATAACTGCTTCTGATGCTTGGAGACCTTATGATGATGATGATGATGATGATGATGATG 661
Db 1614 CTGTGATGCTGCTTCACTGATCTTGGAGAGCTGATGATGATGATGATGATGATGATGATGAT 1673
Qy 662 AGTTGAGCTTGAAGATCTATATAGGCAACTTGGCACTTCTTGGCAAGCTTCTGCTTCTG 721
Db 1674 AGTTGAGCTTGAAGATCTTACAGCCAAATGAGGCTTCTTGGCAAGGCTTCTGCTTCTG 1733
Qy 722 TTGAAGGAAATCCAGAGTGGTGAATCTGAACCTTCTTAAACAGAGAGGTAAGTATATACA 781
Db 1734 ATGGGAAAGGCAAGTGGTGAATCTGAATCTCTCTCAAGGAGAGGTAAGTATATACA 1793
Qy 782 GCTGCACACCTCTGAATCTTCTGATGCTTCAAGGAGAGTAAAGAGACCGATACCA 841

Db 1794 GCTGCAACCCCGGAATCTTCAGTGTCCATACCGGAAGAGCTAAGAGGACAGATACCA 1853
Qy 842 TTTTCTGGCCAGGTTCTCTCTGGTTTAAACGCTGTGGTGGGAACCTGTGCTGTCTCTCC 901
Db 1854 TATTTCTGGCCAGGTTCTCTCTGGTTTAAACGCTGTGGTGGGAATTTGTGCTGTCTCTCC 1913
Qy 902 ACAATTTGCAATGATGTCAATGTGTCCTCAAGCAAGATTTCTAATAAATACACAGAGTCC 961
Db 1914 ATAAATTTGCAATGATGTCAATGTGTCCTCAAGCAAGATTTCTAATAAATACACAGAGTCC 1973
Qy 962 TTCAGTTGAGACCAAGACCGGTGTGTCAGGGGATTTGACAAATCACTCACCCAGCTGGGCC 1021
Db 1974 TTCAGTTGAGACCAAGACCGGTGTGTCAGGGGATTTGACAAATCACTCACCCAGCTGGGCC 2033
Qy 1022 TGAGACCAATGAGGAGTGTGACTGTGTGTCAGAGGGAGACAGAGGATAGCCGCATC 1081
Db 2034 TGGNAACACACAGGAGGATGTGACTGTGTGTCAGAGGGAGACAGAGGATAGCCGCATC 2093
Qy 1082 ACCACAGCAGCTCTTGGCCAGAGCTGTGTCAGGAGTGTGTCAGGAGTGTGTCAGGAGCT 1141
Db 2094 CTTGCTAGCAGCACAG-----TGAGCACTGGCAATCTGTGTACCCCAAGCAAC 2145
Qy 1142 ATGCGTTATCTCATCTTAATCTCAGTTGTTGCTTCAAGACCTTTCATCTCAGGAT 1201
Db 2146 CTTTCATCCCCACAGCGTTGGCCGAGGCTC---TCAGCTGCTGATGCTGGCTATGGT 2201
Qy 1202 TTACAGTGCATTTCTGAAAGAGGAGACATCAAAAGAGATTTAGGAGTTGTGCAACAGCTCT 1261
Db 2202 AAGATCTTACTCGTCTCCAAACAAATTTCTCAGTTGTTGCTTCAATAGCTTCCCTGCT 2261
Qy 1262 TTGAGAGGAGGCTTAAAGGACAGAGGAAAGGCTTCAATCGTGGAAAGAAATTAATG 1321
Db 2262 AGGACTTCAAGTCTCTTCTAAAGACAGAGGACCAAGAGGAGTCAATCAAAAGCACT 2321
Qy 1322 TTGTTATTAATGATCACAGCTAGTTTTCAGAGTTTACCATGTACGTTATTCCTAGCTGG 1381
Db 2322 GCCTCTAGAGGAAGCCAGACAAATGGTCTTCGACCAAGAAATGAATGAT 2381
Qy 1382 GTTCTGTTATTTAGTTCTTTTCGATAGCGCTTAGGTTAATGTGAGTACAGGAAAGAACTG 1441
Db 2382 AGATCGCTAGCAAACTCTGGAGTGACAGCATTTCTTTTCCACTGACAGAAATGGTAGCT 2441
Qy 1442 TGCAAGTGACACCTGATTCGGTTGCTTAACTTAAAGCTTCAATGCTCGGCT 1501
Db 2442 TAGTTGTTGATTTGAGTGGCAAGTGATGTGACACAGAAATGGTGAAGAAACACACTT 2501
Qy 1502 AAAATCGTAAATCTGGATTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTAACC 1561
Db 2502 GATTTGGAACAATGCAGAAA---TACTTGGATTTCTCCAACTGTTTGCATAGATAGACA 2558
Qy 1562 AGAACATTTCTATGTAACAACTGGTTTTTTTAAAGGAACATATGTTGCTATGAAATTA 1621
Db 2559 GATGCTCTGTTTCTACAACTCAAAGCTTTTAGAGGAGCTATGTTAATAGGAATTA 2618
Qy 1622 ACTTGTCTGTCTGATAGACAGACTGGATTTTTTTCATATTTCTTATTAATAATTTCTGCC 1681
Db 2619 A--TGTTCCATGCTGAAGGAAGAGCTGAAGTTTTCAA--TGCTTGGCAACTTCTCCGCA 2674
Qy 1682 ATTTAGAGAGAGAACTACATTCATGTTTGAAGAGATAAACCTGAAAGAGAGTGG 1741
Db 2675 ATTTGAGAGAGAG---TGCGGTCAATGTTTGAAGAGACACCTGACAGAGAGTGG 2731
Qy 1742 CTTTATCTTCACTTTATCGATAAGTCAAGTTATTTGTTTCATGTGTACATTTTATATTT 1801
Db 2732 CTTTCCCTTC-CCTTCCCTCTGAGGGGCTTCTGTGTTTCAATGTGTATATTTTATATTT 2790
Qy 1802 CTCCTTTTGACATTAATCTGTTGGCTTTTCTAATCTTGTAAATATATCTATTTTATCC 1861
Db 2791 CTCCTTTTGACATTAATCTGTTGGCTTTTCTAATCTTGTAAATATTTCTATTTTATCC 2850
Qy 1862 AAAGGTATTTAATATTTCTTTTATGACAACTTAGATCAACTATTTTATGCTTGGTAA-- 1919
Db 2851 AAAGGTATTTAATATTTCTTTTATGACAACTTAGAGCAATTTATTTTATGCTTGTATTT 2910

RESULT 9

US-09-706-968-42
; Sequence 42, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastaSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 3571
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1049)...(2086)
US-09-706-968-42

Query Match 45.5%; Score 959.4; DB 4; Length 3571;
Best Local Similarity 70.3%; Pred. No. 6.4e-235;
Matches 1446; Conservative 1; Mismatches 578; Indels 31; Gaps 11;

Qy 2 CCGCCCGTGAAGTGAAGTCTCACCCAGTCAAGCAATGAGCCTCTTCGGGCTTCTCCTGG 61
Db 1014 CCGCCCGTGAAGTGAAGTCTCACCCAGTCAAGCAATGAGCCTCTTCCTCGGCTTCTCCTGC 1073
Qy 62 TGACATCTGCCCTGGCGGCGGCGAGAGGAGGAGTCAAGGGAATCCAACTGAGTAGTA 121
Db 1074 TGACATCTGCCCTGGCGGCGGCGGAGAACCGGGGAGTCCGAGTCAAGTCCAACTGAGAGCA 1133
Qy 122 AATTCAGATTTTCCAGCAACAAGGAAACAGAACGAGTCAAGATCCTCAGCATGAGAGAA 181
Db 1134 AGTTGAGCTCTCCAGCAACAAGGAAACAGAACGAGTCAAGATCCTCCGCGATGAGAG 1193
Qy 182 TTATTTCTGTCTCTAATATGGAAGTATTCACAGCCCAAGGTTTCTCTATCTATCTCAA 241
Db 1194 TTGTCTATATCTGTTAATGAGAGATCCACAGCCCGAAGTTTCTCTCATATACCCAA 1253
Qy 242 GAAATACGGTCTTGGTATGGAGATTTAGTACAGTACAGGAAATGATGATGATACAACTTA 301
Db 1254 GAAATATGGTCTGGTGTGGAGATTTGAGTATGATGATGATGATGATGATGATGATGATGAT 1313
Qy 302 CGTTTGAAGAAATTTGGGCTTGAAGACCCAGAGATCAATATGATGATGATGATGATGATGAT 361
Db 1314 CAITTCATGAGATTTGGGCTTGAAGATCCAGAGCAGATATATGCAAGTATGATGATGATGAT 1373
Qy 362 TAGAGTTGAGGAAACCACTGATGAGTATATATTTAGGCGCTGCTGCTGCTGCTGCTGCTGCT 421

1374	DB	TAGAA	TTGAGGAGCCCGATGATGGAA	GTGTTTTAGGACGCTGGTGTGGTTCTGGGAC	TG	1433	
422	QY	TAC	CAGGAAAA	CAGATTTCTAAAGGAAATCAA	AATTAGGATAAGATTTGTATCTGATGAAT	481	
1434	DB	TGC	AGAAAGCAGAC	CTTCTTAAAGGAAATCATATC	ACGATAAGATTTGTATCTGATGA	1493	
482	QY	ATTTT	CTCTGAAACAGAGG	TTCTGCATACACTACAA	CATTGTTCATGCCACAATTCACAG	541	
1494	DB	ATTTT	TCATCTGAA	CCCGATTCTGATCCACT	TACAGTATTATCATGCCCACAAGTCACAG	1553	
542	QY	AAG	CTGTGAGTCC	TTTCAAGTACCCCTTCAG	CTTTGCGCATCTGGACCTGTCTTAATAATG	601	
1554	DB	AAA	CCACGAGTCC	TTTCCGCTTCATCTTTGT	CATTGGACCTGCTCTCAACAATG	1613	
602	QY	CTATA	CTGCTTTAGTAC	CTTCTGGAAGACCTTATTC	GCATATCTTGAACACAGAGATGCG	661	
1614	DB	CTGT	GACTGCTTCAGTAC	CTTCTGGAAGAGCTGATTC	GGTACCTAGAGCCAGATCGATGCG	1673	
662	QY	AGT	TGGACTT	AGAGATCTATATAGG	CAACTTTGGCAA	CTTCTTTGGCAAGGCTTTTGT	721
1674	DB	AGG	TGGACTTTG	GACAGCCTCTCAAG	CCAACTTTGGCAGCTTTTGGGCAAGGCTTT	1733	
722	QY	TTG	AGAAAAAT	CCAGAGTGGTGCATCTG	AACCTTTAA	CAGAGGAGTAAAGATTATACA	781
1734	DB	ATG	GA	AAAAAAGCA	NAAGTGTGAATCTCT	CTCAGGAAGAGGTA	1793
782	QY	GCT	GCACACTCT	GTAACTTCTCAGTCT	CCATATAGGAGAGAACTTA	AGAGAACCGATACCA	841
1794	DB	GCT	GCACACCCCG	AACTTCTCAGTGTCC	ATACGGGAAGAGCTTAA	AGAGACAGATACCA	1853
842	QY	TTT	CTGGCCAGGTTGT	CTCCTGGTAAAA	CGCTGTGTGGGAACTGT	GCCTGTGTGTCTCC	901
1854	DB	TAT	CTGGCCAGGTTGT	CTCCTGTCAAG	CGCTGTGGAGAAATTTGT	GCCTGTGTGTCTCC	1913
902	QY	ACA	ATTGCCAATGAATGT	CTCAATGTGCC	ACAGAACTTCTAA	AAAAATACCA	961
1914	DB	ATA	ATTGCCAATGAATGT	CTCAGTGTCC	ATACGGGAAGTTC	AAAAAGTACATGAGGTCC	1973
962	QY	TT	CAGTTGAGACAA	AGACCGGTGTCA	GGGATTTGCAAAATCACT	CACCGACGTGGCCC	1021
1974	DB	TT	CAGTTGAGACAA	AAAACTGGAGTCA	AGGATTTGCATAAGTCACT	CACTGTGTGGCTC	2033
1022	QY	TG	GACCACTAGGAGTGT	CACTGTGTGCGAG	GGGACACAGGAGGATAC	CCGATC	1081
2034	DB	TG	AAACACACGAGGAATG	ATGATCTGTGTAG	AGAAACGACGAGGAGTAACT	CGAC	2093
1082	QY	ACC	ACACGAGCTCTTCC	CCAGAGCTGTGCAGT	GCAGTCTTCTATTAG	AAACGT	1141
2094	DB	CTT	CGTAG	CA	CACTGCTGTATCC	CCCAACAGCAAC	2145
1142	QY	AT	GCTTATCTCCATCT	TAACTCAGTGT	TTGCTTCAAGGACCTTTCACT	CTCAGGAT	1201
2146	DB	CTT	CATCCCAACAGG	TTGGCC	CCAGGCTC-----TCAGCTGCTGATGCTGGCTATGGT	2201	
1202	QY	TT	CAGTGCATCTTGA	AAAGGAGACATCAA	ACAGAAATTAGGAGTGTGTG	CAACAGCTCTT	1261
2202	DB	AAA	GATCTTACTCGTCT	CCAACTTCTCAGT	TTGTGCTTCAATAG	CTCTCCCTGCG	2261
1262	QY	TT	GAGGAGGSCCTTAA	AGGACAGAGAAAAAGTCTT	CAATCTGTGGAAGAAAAATTAATG	1321	
2262	DB	AG	ACTTCAAGTGTCTT	TAAGACCCAGGACCA	AGGAGTCAATCA	AAAGCACT	2321
1322	QY	TT	GATTAAATAGATCA	CCAGTCTAGTTT	TCAGAGTTACA	TGTATCCACT	1381
2322	DB	GC	TTCTAGAGGAAGCC	CAGACAATATGTTCT	CTGACCACAAAACAAATGAATGT	2381	
1382	QY	GTT	CTGTATTTT	CAGTCTCTTCGATAC	CGGCTTAGGTAATGTCA	TACAGGAAAAAACTG	1441
2392	DB	AGA	TCGCTAGCAAACT	CTGGAGTGCAGCA	TTCTTTTCCACTGC	ACAGATGGTGTAGCT	2441
1442	QY	TG	CAAGTGAGCAC	CTGTATTCGTTT	CGCTTTAACTCTAA	AGCTCAATGTCTTGCGCT	1501
2442	DB	TAG	TTGTCTGATATGG	CAAGTGTGTGAC	CAACAGAAATTGTGT	AAAAACACACTT	2501

Qy	1502	AAATCGTATAAACTCGGATTTTTTTTTTTTGGTCTAATTCACATATGTAAC	1561
Db	2502	GATTGTGAACAATGCGAGAAA--TACTTGGATTCTTCCAACCTGTTTGCATAGATAGACA	2558
Qy	1562	AGAACATTCTATGTACTACAAACCTGGTTTTTAAAGGAACATATGCTGTGAATTA	1621
Db	2559	GATGCTCTGTTTCTTCAAACTCAAGCTTTTAGAGCAGCTATGTTTATAGGAATTA	2618
Qy	1622	ACTTGTGTCRTGCTGTATAGACAGACTGGATTTTTTCATATTTCTTATTAAAAATTTCTGCC	1681
Db	2619	A--TGTGCCATGCTGAAGGAAGACTGAAGTTTCAA--TGCTTGGCAACTTCTCCGCA	2674
Qy	1682	ATTAGAAGAGAGAACTACATTCATGTGTTTGAAGAGATAAACCTGAAAGAGAGTGG	1741
Db	2675	ATTGGAGGAAAGG--TGCGGTCATGGTTTGAGAGAAAGCACACCTGCGCAGAGGAGTGG	2731
Qy	1742	CCATATCTCACATTTATCGATAGTCAGTTTATTTGTTTCATTGTCTACATTTTATATT	1801
Db	2732	CCATCCCTC-CCTCCCTCTGAGGTGGCTTCTGTTTCAATTTGCTATATTTTATATT	2790
Qy	1802	CTCCTTTTGACATTATAACTGTGTGGCTTTTCTAAATCTGTTAAATATATCTATTTTACC	1861
Db	2791	CTCCTTTTGACATTATACTGTGTGGCTTTTCTAAATCTTGTAAATATTTCTATTTTACC	2850
Qy	1862	AAAGGTATTTAATATCTTTTTTATGACAACTTAGATCAACTATTTTACCTTGGTAA--	1919
Db	2851	AAAGGTATTTAATATCTTTTTTATGACAACTTAGAGCAATTTATTTTACCTTGTAAATT	2910
Qy	1920	-ATTTTCTTAAAACAACTGCTTATAGCCGAGGAAACAAGATG--GATATATAAAATATT	1975
Db	2911	TTTTTTTCTTAAAACAATTTGTTATAGCCGAGGAAACAAGATGTTGATATAAAATCTTT	2970
Qy	1976	GTTGCCCTGGCAAAAAATACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAAA	2035
Db	2971	GTTGCTCT-GACAAAACAATATGATTT-CTTCTTGTATGGTCTAGAGCTTAGCGTCA	3028
Qy	2036	CTTGCATTTTAAAAA	2051
Db	3029	TCTGCATTTGAAAAGA	3044

```

RESULT 10
US-09-457-066-42
; Sequence 42, Application US/09457066
; Patent No. 6433673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZYGEF33
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 3571
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1049) ..(2086)
US-09-457-066-42

```

Query Match 45.5%; Score 958.4; DB 4; Length 3573;
Best Local Similarity 70.5%; Pred. NO. 1.2e-234;
Matches 1450; Conservative 2; Mismatches 575; Indels 29; Gaps 12;

Db 2442 TAGTTGTC TTGATATGGCAAGTGATGTCAGCACAGAAATGGTGAAACACACACTT 2501

QY 2 CCGCCGTGAGTCTTCAACCCAGTCAAGCAATGAGCCTCTTCGGGCTTCTCTGG 61
Db 1014 CCGCCCGAGTGAGCCCTGGCCCGAGTCAGCCAAATGCTCTCTCTCGGCTCTCTCTGC 1073
QY 62 TGACATCTGCTGCGCGCCAGAGCGAGGAGTCTCAGCGGAATCCACCTGAGTGA 121
Db 1074 TGACATCTGCTGCGCGCCAGAGCGAGGAGTCTCAGCGGAATCCACCTGAGTGA 1133
QY 122 AATTCAGTTTCCAGCAACAGGAACAGAACCGAGTCAAGATCTCTCAGCATGAGAGAA 181
Db 1134 AGTTGAGCTCTCCAGCGACAGGAACAGAACCGAGTCAAGATCTCCGCGCATGAGAG 1193
QY 182 TTATTAATCTGCTCTACTAAATGGAAGTATTCAGAGCCCAAGTTTCTCTACTATCCAA 241
Db 1194 TTGTCATATATCTGGTAATGGAGCATCCAGAGCCCGAAGTTTCTCTATACATACCAA 1253
QY 242 GAAATACCGTCTTGGTATGAGATTAAGTAGCAGTAGAGGAAATATGATGGATCAACTTA 301
Db 1254 GAAATATGGTCTGGTGTGGAGATTAAGTAGCAGTAGAGGAAATATGATGGATCCAGCTGA 1313
QY 302 GATTGATGAAGTTTGGCTTGAGACCCAGAGATGACATATCAGAGTATGATTTG 361
Db 1314 CATTTGATGAGATTTGGCTGGAAGTCCAGAGCCAGATATATCAAGATGATTTG 1373
QY 362 TAGAAGTTGAGGAAACCCAGTATGAACTATATAGGGCGCTGGTGTCTCTGTAATG 421
Db 1374 TAGAAGTTGAGGAGCCAGTATGAAAGTGTTTAGGACGCTGGTGTCTCTGTAATG 1433
QY 422 TACAGAAACAGATTTCTAAAGGAATCAATATAGGATAGATTTGATCTGATGAAT 481
Db 1434 TGCCAGGAAACAGACTTTCTAAAGGAATCAATATAGGATAGATTTGATCTGATGAAT 1493
QY 482 ATTTTCCTCTGAACAGAGGTTCTGCATCCACTACACATTTGTCATGCCACAAATCACAG 541
Db 1494 ATTTTCATCTGAACCGGATTTCTGCATCCACTACAGTATATCATGCCACAGTACAG 1553
QY 542 AAGCTGTGAGTCTTCAAGTCTGACCCCTTCAAGCTTGCATGAGAGCTGCTTAATATG 601
Db 1554 AAACACAGAGTCTCTCGGTTGCGCCCTTCTATCTTGTGATGGACCTGCTCAACAATG 1613
QY 602 CTATACTGCTTTAGTACCTTGAAGACCTTATCTGATATCTTGAACAGAGAGATGCG 661
Db 1614 CTGTGACTGCTTCAAGTACCTTGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGCG 1673
QY 662 AGTTGAGCTTAGAAGATCTATATAGGCAACTTGGCAACTTCTTGGCAAGGCTTTTGT 721
Db 1674 AGTGGACTTGGACAGCTCTCAAGCCAACTAGGAGCTTTTGGCAAGGCTTTCTCTGT 1733
QY 722 TTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTTAAACAGAGAGTAAAGATTACA 781
Db 1734 ATGGGAAGAAAGCAAGTGGTGAATCTGAATCTCTCAAGGAGAGTAAACTTACA 1793
QY 782 GCTGCACACTGTGAATCTTCAAGTCTCAATAGGGAAGAACTAAAGAGAACCGATACCA 841
Db 1794 GCTGCACACCCCGAATCTTCAAGTCTCAATAGGGAAGAACTAAAGAGAACCGATACCA 1853
QY 842 TTTTCTGCGCAGGTTGTCTCTGTTTAAAGCTGTGGTGGAACTGTGCTGTGCTCC 901
Db 1854 TATTCTGCGCAGGTTGTCTCTGTTTAAAGCTGTGGTGGAACTGTGCTGTGCTCC 1913
QY 902 ACHATTGCAATGATGTCAATGTCTCCAGAGAAAGTTTCTTAAAGAAATCCAGAGGTC 961
Db 1914 ATAAATGCAATGATGTCAATGTCTCCAGAGAAAGTTTCTTAAAGAAATCCAGAGGTC 1973
QY 962 TTCAATTTGAGACCAAGAGCCGTTGTGAGGGAATGACAAATCACTCCAGAGGTC 1021
Db 1974 TTCAATTTGAGACCAAGAGCCGTTGTGAGGGAATGACAAATCACTCCAGAGGTC 2033
QY 1022 TGGAGCCATAGGAGTGTGATGTGTGTGAGAGGAGCCACAGAGGATAGCCGATC 1081
Db 2034 TGGAAACACAGAGGAATGTGATGTGTGTGAGAGGAACAGAGGAGTAACTTAACTGCAGC 2093
QY 1082 ACCACAGAGCTCTTTGCCCGAGAGCTGTGAGTGCAGTGGCTGATTTCTATTAGAGAACGT 1141

Db 2094 CTTCTGAGCAGCAC---ACGTGAGCCTGGCATTTCTGTGTACCCCLYACAAGCAACCTT 2150
QY 1142 ATGGGTTATCTCCATCTTAATCTCAGTTGTTGCTTCAAGGACCTTTTATCTTCAAGAT 1201
Db 2151 ---CATCCCAACAGAGTGGCCGAGGGCT---CTCAGCTGCTGATGCTGGCTATGCT 2203
QY 1202 TTACAGTGCATTTCTGAAGAGGAGACATCAAAAGAAATTAGGAGTTGTGCAACAGCTCTT 1261
Db 2204 AAAGATCTTACTCTCTCCCAACCAAAATTTCTCAGTTGTTGCTTCAATAGCTTCCCTGTC 2263
QY 1262 TTGAGAGAGGCTTAAAGGACAGAGAGAGGCTTCTCAATCTGTGGAAGAAATTAATG 1321
Db 2264 AGGATCTCAAGTGTCTTAAAGACAGAGGACCAAGAGGAGTCAATCAACAAGCACT 2323
QY 1322 TTGTAATTAATAGATCACAGCTAGTTTTCAGAGTTTACCATGTACGTAATTTCCACTAGCTGG 1381
Db 2324 GCCTTCTAGAGGAAGCCAGACAAATGCTTCTGACCAAGAAACAAATGAATGAATGT 2383
QY 1382 GTTCTGTATTTCTGATCTTTCGATACGGCTTAGGGTAAATGTGAGTACAGGAAAAAAGCTG 1441
Db 2384 AGATCGCTAGCAACTCTGAGGTGACAGCAATTTCTTTCACCTGACAGAAATGGTGTAGCT 2443
QY 1442 TGCAAGTGAGCACCTGATTCCTGCTTGCCTTAACTCTAAAGCTCCATGTCTCTGGGCT 1501
Db 2444 TAGTTGCTTGTATGATGGCAAGTGTGACGACAAAGAAATGGTGAAAGAAACACACACTT 2503
QY 1502 AAAATCGTATAAATCTGGAATTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTAAC 1561
Db 2504 GATTTGAAACATGCAAGAA---TACTTGGATTTCTCCAACTGTTTGCATAGATAGACA 2560
QY 1562 AGAATCTTATGATGACTACAAACCTGTTTAAAGAGAACTATGTTGCTATGAATTA 1621
Db 2561 GATGCTCTGTTTCTACAACTCAAGCTTTTGAAGAGCAGCTATGTTAATAGGATTA 2620
QY 1622 ACTTGTCTGTGATGATGAGCAGCTGATTTTTCATATTTCTTATTTAAATTTCTGCC 1681
Db 2621 A--TGTCCTGCTGTAAGGAAAGACTGAAAGTTTTCAA--TGCTTGGCAACTTCTCCGCA 2676
QY 1682 ATTTAGAAGAGAACTACATTCATGTTTGAAGAGATAAACCTGAAAGAGAGTGG 1741
Db 2677 ATTTGAGAGAAAGS---TGCGGTCTGTTTGAAGAGCAGCACTGACAGAGAGTGG 2733
QY 1742 CTTATCTTCACTTATGATTAAGTCAAGTTTATTTGTTTCAATTTGTTGTTGTTTATTTATTT 1801
Db 2734 CTTCCCTTC--CCTTCCCTCTGAGGTGGCTTCTGTTTCAATTTGTTATATTTTATTT 2792
QY 1802 CTCCTTTTGACATTAATACTTGGCTTTTCTAATCTTGTAAATATATCTATTTTACC 1861
Db 2793 CTCCTTTTGACATTAATACTTGGCTTTTCTAATCTTGTAAATATTTCTATTTTACC 2852
QY 1862 AAAGGATTTAATTTCTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGGTAA-- 1919
Db 2853 AAAGGATTTAATTTCTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGGTAA-- 2912
QY 1920 -ATTTTCTTAAACACAACTTGTATAGCAGAGGAAACAAAGATG---GATATAAATAATTT 1975
Db 2913 TTTTCTTAAACAAATTTGTATAGCAGAGGAAACAAAGATGATTTGATATAAATAATTT 2972
QY 1976 GTTGCCTTGACAAAAATACATATNTCCATCCCGAATGGTGTGATGATTTAA 2035
Db 2973 GTTGCCTT--GACAAAAACATATGATTT--CTTCTTGTATGGTGTGATGAGCTTAGCGTCA 3030
QY 2036 CTTGCAATTTTAAAAA 2051
Db 3031 TCTGCAATTTGAAAGA 3046

RESULT 11

US-09-457-066-6

; Sequence 6, Application US/09457066

; Patent No. 6435673

; GENERAL INFORMATION:


```

; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1035)
; OTHER INFORMATION: n = A,T,C or G
US-09-457-066-6

Query Match          34.8%; Score 734.4; DB 4; Length 1035;
Best Local Similarity 56.6%; Pred. No. 8.9e-178;
Matches 585; Conservative 261; Mismatches 188; Indels 0; Gaps 0;

QY 37 ATGAGCCTCTTCGGGCTTCTCCTGGTGCATCTGCGCCGCGCAGAGAGAGGAGT 96
DB 1 ATGWSNYTNTYGGNYTNTYNTYNTACNWSNGCYNTGNCNGNCARMGNCARGNACN 60
QY 97 CAGCGGAATCCACCTGAGTAGTAATCCAGTTTCCAGCAACAGGAAACAGACGA 156
DB 61 CAGCNGARWSNAAYYTNWSNNAARTTYCARTTYWSNWSNAAYAARGARCARAYGN 120
QY 157 GTACAAGATCTCAGCATGAGAGAAATTAATCTGTCTACTAATGGAAGATTTCACAGC 216
DB 121 GTNCARGAYCCNARCAYGARMGNATHACNGTNWSNACNAAYGWNWSNATHCAYWSN 180
QY 217 CCAGGTTTCTCATATCTTCCAGAAATACCGTCTTGATGAGAGATTAGTAGCAGTA 276
DB 181 CCNMGNTTCCNCAATCAATCCAGNAAATACNGNAAATACNGNAAATACNGNAAATACNGN 240
QY 277 GAGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 336
DB 241 GARGAAYGNTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 337 GATCAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 396
DB 301 GAYGAYATHTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 397 GGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 456
DB 361 GGNMGNTGGTGGGNGNGNACNGTNCNGNACNGTNCNGNACNGTNCNGNACNGTNCNGNACNGT 420
QY 457 AGGATAGATTTGATCTGATGATATTTCTCTGATGATGATGATGATGATGATGATGATGAT 516
DB 421 MGNATHMGNTTGTGNTGNSGAYGATATTTCCNWSNGARCCNGNTTGTGATGATGATGAT 480
QY 517 AACATTTGATGCCACATTCACAGAAAGCTGTGAGTCTTTCAGTGTGATGATGATGATGATGAT 576
DB 481 AAYATHGNTATGCCNARTTYACNGAGCNGTNCNWSNCCNWSNCCNWSNCCNWSNCCNWSNCCN 540
QY 577 TTGCCACTGGACCTGCTTAATATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 636
DB 541 YTNCCNYTNGAYYNTYNTAAAYGNCNATHACNGCNYTWSNACNYTWSNACNYTWSNACNYT 600
QY 637 CGATATCTTGAACACAGAGATGCGAGTTGAGTCTAGAGATCTATATAGGCGCAACTGG 696
DB 601 MGNATYTNARCCNGARMGNTGTCARYTNGAYTNGAYTNGAYTNGAYTNGAYTNGAYTNGAYTNG 660

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QY 697 CAACCTTCTGGCAAGGCTTTGTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTT 756
DB 661 CARYTNTYNGGNAARGCNTTYGNTTYGNGMGAARWSNMGNGTNGTNGAYYTNAAAYTN 720
QY 757 CTAAACAGAGAGGTAAAGATTATACAGCTGCACACCTCGTAACCTCTCAGTGTCCATAAGG 816
DB 721 YTNACNGARGAGTNGMNTNTAYNSNTGYACNCCNMGNAAATTTWSNGTNSNATHMGN 780
QY 817 GAAGAACTAAAGAGAACCGATACCAATTTCTGGCCAGGTTGTCTCTGTTAAACCGCTGT 876
DB 781 GARGARYTNARMENACNGAYACNAHTTCTGCCCNGGNTGYTNTYNTGNTNAARMGNTGY 840
QY 877 GGTGGGAACTGTGCTGTTGTCTCCCAATTCGATGATGATGATGATGATGATGATGATGATG 936
DB 841 GNGGNAAYTGYGNTGYTNTCAAYATGYTAYGARTGYCARTGYTNCNWSNAAAR 900
QY 937 GTTACTAAATAATACCACGAGGTCTCTCAGTTGAGACCAAGACCGGTGTCCAGGAGATTG 996
DB 901 GTWACNDARAARTAYCAYGARTGYTNCARYTNMGNCCNAAACNGGNTNMGNNGYTN 960
QY 997 CACAAATCTACCGAGCTGGCCCTGGAGCACCATGAGAGTGTGACTGTGTGTCAGA 1056
DB 961 CAYAAARWSNYTNACNGAYTNGCNYTNGARCAAYCAYGARGARTGYGTYGTYGTYGTYG 1020
QY 1057 GCGAGCACAGGAGG 1070
DB 1021 GGNWSNACNGGNGG 1034

RESULT 12
US-09-706-968-6
; Sequence 6, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
; PRIOR FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: degenerate sequence derived from SBQ ID NOS: 1 and
; OTHER INFORMATION: 2
; NAME/KEY: misc_feature
; LOCATION: (1)...(1035)
; OTHER INFORMATION: n = A,T,C or G
US-09-706-968-6

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Query Match          34.8%; Score 734.4; DB 4; Length 1035;
Best Local Similarity 56.6%; Pred. No. 8.9e-178;
Matches 585; Conservative 261; Mismatches 188; Indels 0; Gaps 0;

QY 37 ATGAGCCTCTTCGGGCTTCTCCTGGTGCATCTGCGCCGCGCAGAGAGAGGAGT 96
DB 1 ATGWSNYTNTYGGNYTNTYNTYNTACNWSNGCYNTGNCNGNCARMGNCARGNACN 60
QY 97 CAGCGGAATCCACCTGAGTAGTAATTCAGTTTCCAGCAACAGGAAACAGACGA 156
DB 61 CARGCNGARWSNAAYYTNWSNNAARTTYCARTTYWSNWSNAAYAARGARCARAYGN 120

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157 GTACAAGATCTCAGCATGAGAGATTAATTAATCTGTCTACTAATGAAAGTATTCACAGC 216
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Qy 217 CCAAGGTTTCTCTATCTATCCAGGAAATACCGTCTTGGTATGAGAGATAGTAGAGTA 276
Db 181 CCNNGNTTYCCNCAAYCAYCNCNMGNAAYACNGTNTYNTGNGMNTYNTGNGCNGTN 240
Qy 277 GAGGAAATGTATGGATCAACACTTACGTTTGCATGAAAGATTTCGGGTTGGAAGACCCAGAA 336
Db 241 GARGAAYGNTGGAHCACTYACNTTYGAYGARMGNTTYGNTNGARGAYCCNGAR 300
Qy 337 GATGACATATGCAAGATGATTTTGTAGAGATTTGAGGAAACCCAGTATGAGAACTATTA 396
Db 301 GAYGAYATHTGYAARTAYGATTTGTNGARGTNGARGARCCNWSNGNACNAATHYTN 360
Qy 397 GGGCGCTGGTGGTCTCTGCTACTGTACCAAGGAAACAGATTTCTAAAGGAAATCAAAIT 456
Db 361 GGNMGNTGGTGGGNGNACNGTNCNGNARCARATHSNARAGGNAAYCARATH 420
Qy 457 AGGATAGATTTGTATCTGATGATATTTCTCTGCTGCAACAGGGTCTGCACTCCACTAC 516
Db 421 MGNATHMGNTTYGNTWSNGAYGARTATTTCCNWSNGARCCNGGNTTGTGATHTCAATY 480
Qy 517 AACATTGTGATGCCACCAATTCACAGAGCTGTGAGTCTCTCAGTGCTACCCCTTCAGCT 576
Db 481 AAYATHGNTATGCCNARTYACNGARGGNTWNSCNNGNTYNTCCNWSNGCN 540
Qy 577 TTGCACTGGACCTGCTTAATATGCTATTAATCTGCTCTTGTAGTCTGGGAGACCTTAT 636
Db 541 YTNCCNVTNGAYTYNTYNAAYAGCNATHACNGCNTTYNSNACNTYNTNGARGAYTYNATH 600
Qy 637 CGATATCTTGAACAGAGAGATGCGAGTTGGACTTAGAAGATCTATATAGGCCAACTTGG 696
Db 601 MNTAYTYNGARCCNGARMGNTGGARYTNGAYTYNGARGAYTYNTAYMGNCCNACNTGG 660
Qy 697 CAATCTCTGGCAAGGCTTTGTTTGTGGAGAAATCCAGAGTGGTGGATCTGAACCTT 756
Db 661 CARVTNTNGNAARGCNTTYGNTTYGGNNGNAARWSNMGNTGNGAYTYNTAAYTYN 720
Qy 757 CTAACAGAGAGGTAAGATTAACAGCTGCACACTCTGTAACCTCTCAGTGTCCATAAGG 816
Db 721 YTNACNGARGGNTMGNNTYNTAYWSNTGYACNCCNMGNAAYTYTWSNGTNSNATHMGN 780
Qy 817 GAAGAACTAAAGAGAACGATACCAATTTCTGGCCAGGTTGTCTCTGGTTAAACCGCTGT 876
Db 781 GARGARYTNAARMGNACNGAYACNATHTTTGTGGCCNGGNTGYTYNTNGTNAARMGNTGY 840
Qy 877 GGTGGAACTGCTGCTGTCTCCCAATTTGCAATGCAATCTCAATGTCCTCCCAAGCAA 936
Db 841 GNGGNAAYTYGCGNTGYTYTTCVCAAYTYGYAAYGARTGYCARTGYTNCNWSNAAR 900
Qy 937 GTTACTAAATAATACCAAGAGTCTCTCAGTTGAGACCAAGACCGGTGTGAGGGGATTG 996
Db 901 GTNACNAARAARTAYCARGAGTNTYNTCARVTNMGNCCNARACNGGNTMNGNGNTN 960
Qy 997 CACAAATCACTCACCGAGTGGCCCTGAGACCACTGAGGAGTGTGCTGTGTGCGAGA 1056
Db 961 CAYARWNSNTYNTACNGAYTGNGNTYNGARCAAYCAYGARGARTGYGATYGTNTGYMGN 1020
Qy 1057 GGGAGCAYCAGGAGG 1070
Db 1021 GGNWSNACNGGNGG 1034

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RESULT 13

US-09-564-595D-6

; Sequence 6, Application US/09564595D

; Patent No. 6495668

; GENERAL INFORMATION:

; APPLICANT: Gilbert, Teresa

; APPLICANT: Hart, Charles E.

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; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: degenerate sequence
; NAME/KEY: misc feature
; LOCATION: (1)-(1110)
; OTHER INFORMATION: n = A,T,C or G
US-09-564-595D-6

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Query Match 8.4%; Score 177.6; DB 4; Length 1110;

Best Local Similarity 34.5%; Pred. No. 8.2e-36;

Matches 349; Conservative 194; Mismatches 395; Indels 75; Gaps 6;

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Qy 118 AGTAATTCACGTTTCCAGCAACAGGACAGACGAGTACAGATCCTCAGCATGAG 177
Db 100 MGNAAAGCNAAAYTNMGMNGAYGARWSNAAAYCAITYTNACNGAYTYNTAYMGMNGAY 159
Qy 178 AGAATTAATTAATCTGCTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCTCATCTAT 237
Db 160 GARACNATHCARGTNAARGGNAAYGNTAYGTNCARWSNCCNMGNTTYCCNAAWWSNTAY 219
Qy 238 CCAAGAAATACGCTCTGCTGATGAGATTAAGTACAGTACAGTACGAGAAATGATGATGATA 297
Db 220 CCNMGNAAYTYNTYNTNACNTGGMNTYNTCAWWS---NCARGAARAYACNMGNATHCAR 276
Qy 298 CTTAGCTTGTGATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGAT 357
Db 277 YTNGTNTTYGAYAAVCARTTYGNTNGARGCNGARGAAYGAYATHTGYMGNATYAY 336
Qy 358 TTTGTAAGTTGAGAAACCCAGTGTGGAAC-----TATATTAGGCGCTGTGTGCT 411
Db 337 TTYGTNGARGTNGARGAYATHWSNGARACNWSNACNATHATHMGNMGNTGCTGYG 396
Qy 412 TCTGCTACTGTACCAAGGAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTTGTA 471
Db 397 CAYAARGARGTNCNCCNMGNATHARWSNMGNACNAYCARATHARATHACNTTYAAR 456
Qy 472 TCTGATGAATATTTCTCTTCTGAACCCAGGGTTCTGCATCCACTACAACTTGTGTC----- 525
Db 457 WSNAGAYATYATYTGTCNNAARCCNGGNTTYAARATHTYATYWWSNYTYNGARGAY 516
Qy 526 -----ATGCCACAATTCACAGAGCTGTGAGTCTTCAGTGTCTAC----- 565
Db 517 TTYCARCCNGCNGCNGCNGWSNGARACNAAAYTGGGARGWSNGTNCNWSNATHWSNG 576
Qy 566 -----CCCTTTCAGCTTTGCCACTTGGACCTCTCTTAATAAT 600
Db 577 GTNWSNTAYAAWWSNCCNWSNGTNAACNGAYCCNACNTYNTATHGNCNGAYGVCNTYNGAY 636
Qy 601 GCTATAACTGCTTTAGTACCTTGGAGACCTTATCGATATCTTGAACCCAGAGATGG 660
Db 637 AARATHGNCNGARTTYGAYACNGTNGARGAYTYNTNAAATYATYTYAAYCCNNGARWSNTGG 696
Qy 661 CAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGCTTTTGT 720
Db 697 CARGARGAYTYTNGARAAATATGTATYTYNGAYACNCCNMGNTAYMGNMGNTWWSNTAY 756
Qy 721 TTTGGAAGAAATCCAGAGTGTGATCTGAACCTTCTAAACAGAGGAGTAAAGATTATAC 780

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Db 757 GAYMGNAR-----WSNAARGTNGAYTNGAYMGNYNAAVYAYGAYGAYCNARMGNTAY 810
 Qy 781 AGCTGCACACCTCGTAACCTCTCAGTGTCTCATAAGGAAGAACTAAAGAGAACCGATACC 840
 Db 811 WNTGYACNCCNMGNAAATAYWSNGTNAAYATHMGNARGARYTNAARYTNGNAAVGTN 870
 Qy 841 ATTCTTGGCCAGGTTCTCTCGTTAAAGCTGTGGTGGGAGCTGTGCTGTGTCTC 900
 Db 871 GNTTITTYCCNMGTGTYTNGTNCARMGNTGNGGNNATYTGNGTNGYGNACN 930
 Qy 901 CACAATTCAGTAAGTCAATGTCTCCAGCAAGATTAATAAATAACACAGGTC 960
 Db 931 GTNAAATGGMGNWSNTGACNTGYAAYWSNGNAARACNGTNAARARETAYCAYARGTN 990
 Qy 961 CTTCACTTGAGACC-----AAAGACCGGTGTTCAGGGGATTGCACAAATCACTCACC 1011
 Db 991 YTNCAATTVGACCCNGGNCAYATHAARMGNMGNMGNMGNMGNMGNMGNMGNMGNMGN 1050
 Qy 1012 GACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGAGAGGGAGCAC 1064
 Db 1051 GAYATHCARYTNGAYCAYCARGMGNMGTYGAYTGYATHGYWSNWSNWSNWSNWSNWSN 1103

RESULT 14

US-09-540-224-3
 ; Sequence 3, Application US/09540224
 ; Patent No. 6468543
 ; GENERAL INFORMATION:
 ; APPLICANT: Gilbertson, Debra G.
 ; APPLICANT: Hart, Charles E.
 ; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
 ; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
 ; FILE REFERENCE: 00-28
 ; CURRENT APPLICATION NUMBER: US/09/540,224
 ; PRIOR FILING DATE: 2000-03-31
 ; EARLIER FILING DATE: 2000-02-04
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 1472
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (93)....(1205)
 US-09-540-224-3

Query Match 5.6%; Score 117.8; DB 4; Length 1472;

Best Local Similarity 50.9%; Pred. No. 1.6e-20; Mismatches 402; Indels 75; Gaps 6;

Matches 494; Conservative 0;

Query Match 5.6%; Score 117.8; DB 4; Length 1472;

Best Local Similarity 50.9%; Pred. No. 1.6e-20; Mismatches 402; Indels 75; Gaps 6;

Matches 494; Conservative 0;

Query Match 5.6%; Score 117.8; DB 4; Length 1472;

Best Local Similarity 50.9%; Pred. No. 1.6e-20; Mismatches 402; Indels 75; Gaps 6;

Matches 494; Conservative 0;

Query Match 5.6%; Score 117.8; DB 4; Length 1472;

Best Local Similarity 50.9%; Pred. No. 1.6e-20; Mismatches 402; Indels 75; Gaps 6;

Matches 494; Conservative 0;

Query Match 5.6%; Score 117.8; DB 4; Length 1472;

Best Local Similarity 50.9%; Pred. No. 1.6e-20; Mismatches 402; Indels 75; Gaps 6;

Matches 494; Conservative 0;

Query Match 5.6%; Score 117.8; DB 4; Length 1472;

Best Local Similarity 50.9%; Pred. No. 1.6e-20; Mismatches 402; Indels 75; Gaps 6;

Matches 494; Conservative 0;

Query Match 5.6%; Score 117.8; DB 4; Length 1472;

Best Local Similarity 50.9%; Pred. No. 1.6e-20; Mismatches 402; Indels 75; Gaps 6;

Matches 494; Conservative 0;

Query Match 5.6%; Score 117.8; DB 4; Length 1472;

Best Local Similarity 50.9%; Pred. No. 1.6e-20; Mismatches 402; Indels 75; Gaps 6;

Matches 494; Conservative 0;

Query Match 5.6%; Score 117.8; DB 4; Length 1472;

Best Local Similarity 50.9%; Pred. No. 1.6e-20; Mismatches 402; Indels 75; Gaps 6;

Matches 494; Conservative 0;

Qy 463 AGATTGTATCTGATGAATATTTCTTCTGACCAAGGGTTCTGCTATCTCACTACACATT 522
 Db 540 ACATTAAAGTCTGATGACTACTTTGTGGCAAAACCTGGATTCAGATTTATTATTCAATT 599
 Qy 523 GT----CATGCCCAATTCACAGAGCTGTGAGTCTTCTAGTCTACCCCTTCAGTTT 578
 Db 600 GTGGAAGATTTCCAAACCGGAGCAGCTTCAGAGACCAACTGGGAATCAGTCAAGCTCT 659
 Qy 579 GCCACTGGACCTGCTTA----- 595
 Db 650 TTCTCTGGGGTCTCTATCACTCCATCAATAACGACCCCACTCTCACTGCTGATGCC 719
 Qy 596 ----ATAATGCTATTAACCTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGACCA 651
 Db 720 CTGGACAAACATGTCGCAATTCGATACCGTGGAGATCTACTTAAGCACTTCAATCCA 779
 Qy 652 GAGAGATGGCAGTTGGACTTTAGAAGATCTATATAGGCCAACTTTGGCAACTCTTGGCAAG 711
 Db 780 GTGTCTTGGCAAGATGATCTGGAGAAATTTGTATCTGGACACCCCTCAATTATAGAGCAGG 839
 Qy 712 GCTTTTGTCTTGGCAAGAAATTCAGAGTGTGCTGATCTGAACCTTCTTAACAGAGGAGGTA 771
 Db 840 TCATACCATGATCGA-----AGTCCAAAGTGGACCTGGACAGGCTCAATGATGATGC 893
 Qy 772 AGATTATACAGTGCACACCTCGTAATCTTCTCAGTGTCTCAATAAGGAGAGCACTAAAGAGA 831
 Db 894 AAGCGTTTACAGTTGCACTCCAGGAATCACTCTGTGAACCTTCAGGGAGGAGCTGAAGCTG 953
 Qy 832 ACCGATACCAATTTCTGGCCAGGTTGTCTCTCTGTTTAAACGCTGTGTGGGAACTGTGCC 891
 Db 954 ACCAATGCACTCTTCTTCCACAGATSCCTCTCTGTCAGCGCTGTGTGGTSCAACTGTGT 1013
 Qy 892 TGTGTCTCCCAATTCGAATGCAATGTCTCAATGTCTTCCCAAGCAAAAGTTACTAAAAAATAC 951
 Db 1014 TGGGAACTGTCACTTGGAACTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 1073
 Qy 952 CAGAGGTCTCTCAGTTGAGACC-----AAAGACCGGTGTGAGGAGTGCACAAA 1002
 Db 1074 CATGAGGTATTTGAAGTTTGGAGCTTGGACCTTGGACATTTCAAGAGAAAGGGGCAAGTAAGAATATG 1133
 Qy 1003 TCACTCAGCAGCTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGC 1062
 Db 1134 GCTCTTGTGATATCCAGCTGGATCATCATGAGCGATGTGACTGTATCTGCACTCAAGA 1193
 Qy 1063 ACAGGAGGATA 1073
 Db 1194 CCACCTCGATA 1204

RESULT 15

US-09-564-595D-52

; Sequence 52, Application US/09564595D

; Patent No. 6495668

; GENERAL INFORMATION:

; APPLICANT: Gilbert, Teresa

; APPLICANT: Hart, Charles E.

; APPLICANT: Sheppard, Paul O.

; TITLE OF INVENTION: GROWTH FACTOR ZVEGF4

; FILE REFERENCE: 99-19

; CURRENT APPLICATION NUMBER: US/09/564,595D

; PRIOR FILING DATE: 2000-05-03

; PRIOR APPLICATION NUMBER: US 09/304,216

; PRIOR FILING DATE: 1999-05-03

; PRIOR APPLICATION NUMBER: US 60/164,463

; PRIOR FILING DATE: 1999-11-10

; PRIOR APPLICATION NUMBER: US 60/180,169

; PRIOR FILING DATE: 2000-02-04

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 52

; LENGTH: 1472

; TYPE: DNA

; ORGANISM: Mus musculus

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)...(1205)
US-09-564-595D-52

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Query Match 5.6%; Score 117.8; DB 4; Length 1472;
Best Local Similarity 50.9%; Pred. No. 1.6e-20;
Matches 494; Conservative 0; Mismatches 402; Indels 75; Gaps 6;

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Db 1194 CCACCTCGATA 1204

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DB	303	AACAGCTTACCAGGACCTGCTTCTGACATGGTGGCTCGGTTCC--CCAGGAGAAAACA	359
QY	289	TGGATCAACACTTACGTTTGTATGAAGAAATTTGGGCTTGAAGACCCAGAGATGACATATGC	348
DB	360	CGGATCAACACTGCTCTTTTGACCATCAATTCGGACTAGAGGAACAGAAAATGACATTTGT	419
QY	349	AAGTATGATTTTGTAGAAGTTGAGAAACCCAGATGATGGA--CTATATTAGGGCGC	402
DB	420	AGGTATGATCTTGTGGAAGTTGAAGAGTCTCAGAGAGCAGCACTGTTGTCAGAGGAAGA	479
QY	403	TGGTGTGGTCTCGTACTGTGACACGAGAAACAGATTTCTAAAGAAATCAAAATTAGATA	462
DB	480	TGGTGTGGCCACAAGGAGATCCCTCCAAAGGATACGTCAGAGAAACAACCCAGATTAATAATC	539
QY	463	AGATTTGTATCTGATGATATTTTCTTCTTGAAACAGGGTTCTGCATCCACTACAACATT	522
DB	540	ACATTTAAGTCTGAAGTACTTCTTGTGGCAAAACCTGGATTCAGATTTATTTATTTT	599
QY	523	GT----CATGCCACAATTCACAGAACTGTGAGTCTTTCAGTGTCTACCCCTTCAGCTTT	578
DB	600	GTGGAAGATTTCCAACCGGAAGACGCTCAGAGACCACTGGGAATCAGTCACAAGCTCT	659
QY	579	GCCACTGACCTGCTTA-----	595
DB	660	TTCTCTGGGGTGCTCTATCTCTCCATTAATACGGAACCCACTCTCACTGCTGATGCC	719
QY	596	----ATAATGTATAACTGCTTTAGTACCTTGGAGACCTTATTCGATATCTTGAACCA	651
DB	720	CTGGACAAAACGTGCGCAGAAATCGATACCGTGAAGATCTACTTAAAGCACTTCAATCCA	779
QY	652	GAGAGATCGGAGTTGGACTTAGAGATCTATAGGCCAACTTGGCAACTCTTGGCAAG	711
DB	780	GTGTCTTGGCAAGATGATCTGGAGAAATTTGATCTGGACACCCCTCATTAATAGAGGACGG	839
QY	712	GCTTTTGTTTTGGAGAAAATCCAGAGTGGTGGATCTGAACCTCTTAACAGAGGAGGTA	771
DB	840	TCATACCATGATCGA-----AGTCCAAAGTGGACCTGGACAGGCTCAATGATGATGC	893
QY	772	AGATTTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGGAAGCACTAAGAGA	831
DB	894	AAGCGTTACAGTTGCATCTCCAGGAATCACTCTGTGAACCTCTCAGGAGGAGCTGGAAGCTG	953
QY	832	ACCGATACCATTTTCTGGCCAGGTTGTCTCTCGTGTAAACGCTGTGTGGGAACTGTGCC	891
DB	954	ACCAATGCAGTCTTCTTCCACGATGCCCTCTCGTGCAGCGCTGTGGTGGCACTGTGGT	1013
QY	892	TGTTGTCTCCACAATTTGCAATGAATGTCAATGTGTCCAGCAAGTTCATAAAAATAC	951
DB	1014	TGCGGAACGTGCACTGGAAATGCTTCACATGTCAGCTCAGGGAAGACAGTGAAGAAGTAT	1073
QY	952	CACGAGGTCTTTCAGTTGAGACC-----AAAGACCGGTGTGAGGGATTCACAAA	1002
DB	1074	CATGAGGTTATGCAAGTTTGACCTTGGACATTTCAAGAGAGGGCAAGCTAAGATATG	1133
QY	1003	TCACTCAACGAGTGGCCCTGGAGCAACATGAGAGTGTGACTGTGTGTGCAGAGGAGC	1062
DB	1134	GCTCTGTGTGATATCCAGCTGGATCATCATGAGCGATGTGACTGTATCTGCAGCTCAAGA	1193

GenCore version 5.1.6
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Total number of hits satisfying chosen parameters: 4380138

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2103.6	99.8	2108	14	US-10-131-600-2
3	1979.4	93.9	2825	14	US-10-178-442-1
4	1979.4	93.9	2839	11	US-09-796-753-5
5	1979.4	93.9	2849	10	US-09-978-295A-487
6	1979.4	93.9	2849	10	US-09-978-697-487
7	1979.4	93.9	2849	10	US-09-978-192A-487
8	1979.4	93.9	2849	10	US-09-999-832A-487
9	1979.4	93.9	2849	11	US-09-978-189-487
10	1979.4	93.9	2849	11	US-09-978-608A-487
11	1979.4	93.9	2849	11	US-09-978-585A-487
12	1979.4	93.9	2849	11	US-09-978-191A-487
13	1979.4	93.9	2849	11	US-09-978-403A-487
14	1979.4	93.9	2849	11	US-09-978-564A-487
15	1979.4	93.9	2849	11	US-09-999-833A-487
16	1979.4	93.9	2849	11	US-09-981-915A-487

17	1979.4	93.9	2849	11	US-09-978-824-487	Sequence 487, App
18	1979.4	93.9	2849	11	US-09-918-585A-487	Sequence 487, App
19	1979.4	93.9	2849	11	US-09-978-423A-487	Sequence 487, App
20	1979.4	93.9	2849	11	US-09-978-193A-487	Sequence 487, App
21	1979.4	93.9	2849	11	US-09-999-830A-487	Sequence 487, App
22	1979.4	93.9	2849	11	US-09-978-757A-487	Sequence 487, App
23	1979.4	93.9	2849	11	US-09-978-187B-487	Sequence 487, App
24	1979.4	93.9	2849	11	US-09-978-643A-487	Sequence 487, App
25	1979.4	93.9	2849	12	US-09-978-375A-487	Sequence 487, App
26	1979.4	93.9	2849	12	US-09-978-188A-487	Sequence 487, App
27	1979.4	93.9	2849	12	US-09-978-298A-487	Sequence 487, App
28	1979.4	93.9	2849	12	US-10-137-870-285	Sequence 285, App
29	1979.4	93.9	2849	12	US-10-140-018-285	Sequence 285, App
30	1979.4	93.9	2849	12	US-10-140-021-285	Sequence 285, App
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33	1979.4	93.9	2849	12	US-10-140-807-285	Sequence 285, App
34	1979.4	93.9	2849	12	US-10-140-922-285	Sequence 285, App
35	1979.4	93.9	2849	12	US-10-140-924-285	Sequence 285, App
36	1979.4	93.9	2849	12	US-10-140-926-285	Sequence 285, App
37	1979.4	93.9	2849	12	US-10-141-698-285	Sequence 285, App
38	1979.4	93.9	2849	12	US-10-141-702-285	Sequence 285, App
39	1979.4	93.9	2849	12	US-10-141-704-285	Sequence 285, App
40	1979.4	93.9	2849	12	US-10-142-421-285	Sequence 285, App
41	1979.4	93.9	2849	12	US-10-142-432-285	Sequence 285, App
42	1979.4	93.9	2849	12	US-10-142-767-285	Sequence 285, App
43	1979.4	93.9	2849	12	US-10-143-031A-487	Sequence 487, App
44	1979.4	93.9	2849	12	US-10-143-033-285	Sequence 285, App
45	1979.4	93.9	2849	12	US-10-144-994-285	Sequence 285, App

ALIGNMENTS

RESULT 1

US-09-852-209A-2
; Sequence 2, Application US/09852209A
; Patent No. US20020164687A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/09/852,209A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2108
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (2002)
; OTHER INFORMATION: can be a, c, g or t

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; NAME/KEY: unsure
; LOCATION: (2065)
; OTHER INFORMATION: can be a, c, g or t
; NAME/KEY: unsure
; LOCATION: (2070)
; OTHER INFORMATION: can be a, c, g or t
; NAME/KEY: unsure
; LOCATION: (2089)
; OTHER INFORMATION: can be a, c, g or t
US-09-852-209a-2

Query Match      99.8%; Score 2103.6; DB 10; Length 2108;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCGCGTGTGAGTCTCTCACCCGAGTCCAGCCAAATGAGCCTCTTCGGGCTCTCCTG 60
Db 1 CCCCGCGTGTGAGTCTCTCACCCGAGTCCAGCCAAATGAGCCTCTTCGGGCTCTCCTG 60

QY 61 GTGACATCTGCCCTGGCGGCGGACAGACAGGAGTCTCAGGCGGAAATCCAACTCAGTAGT 120
Db 61 GTGACATCTGCCCTGGCGGCGGACAGACAGGAGTCTCAGGCGGAAATCCAACTCAGTAGT 120

QY 121 AAATTCAGATTTTCCAGCAACAAGAAACAGAACGAGTACAGATCTCTCAGCATGAGAGA 180
Db 121 AAATTCAGATTTTCCAGCAACAAGAAACAGAACGAGTACAGATCTCTCAGCATGAGAGA 180

QY 181 ATATTACTGTCTCTACTTAATGGAAGTATTCCAGAGCCCAAGTTTCTCATCTATATCCA 240
Db 181 ATATTACTGTCTCTACTTAATGGAAGTATTCCAGAGCCCAAGTTTCTCATCTATATCCA 240

QY 241 AGAAATACGGTCTTTGGTATGAGATTTAGTAGCAGTACAGGAGAAATGTATGGATACAACTT 300
Db 241 AGAAATACGGTCTTTGGTATGAGATTTAGTAGCAGTACAGGAGAAATGTATGGATACAACTT 300

QY 301 ACGTTTATGAAAGATTTGGCTTTGAAGACCCAGAGATGACATATGCAAGTATGATTTT 360
Db 301 ACGTTTATGAAAGATTTGGCTTTGAAGACCCAGAGATGACATATGCAAGTATGATTTT 360

QY 361 GTAGAAGTGTAGGAACCCAGTGTGGAACTATATTAGGGCGCTGGTGTGGTCTTGGTACT 420
Db 361 GTAGAAGTGTAGGAACCCAGTGTGGAACTATATTAGGGCGCTGGTGTGGTCTTGGTACT 420

QY 421 GTACAGAGAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTTGTATCTGATGAA 480
Db 421 GTACAGAGAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTTGTATCTGATGAA 480

QY 481 TATTTTCTCTGAAACCAAGGTTCTGCATCCACTACACATTTGTCATGCCACAAATTCACA 540
Db 481 TATTTTCTCTGAAACCAAGGTTCTGCATCCACTACACATTTGTCATGCCACAAATTCACA 540

QY 541 GAAAGCTGTGATCTCTCAGTGTCTACCCCTTTGACCTTTGACCTGACCTGCTTAATAAT 600
Db 541 GAAAGCTGTGATCTCTCAGTGTCTACCCCTTTGACCTTTGACCTGACCTGCTTAATAAT 600

QY 601 GCTATAACCTGCTTAGTACCTTGGAGAACCTTATTCGATCTTTGAAACCAAGAGATGG 660
Db 601 GCTATAACCTGCTTAGTACCTTGGAGAACCTTATTCGATCTTTGAAACCAAGAGATGG 660

QY 661 CAGTTGACCTTAGAAGATCTATATAGGCCCACTTGGCACTTCTTTGGCAAGGCTTTTGT 720
Db 661 CAGTTGACCTTAGAAGATCTATATAGGCCCACTTGGCACTTCTTTGGCAAGGCTTTTGT 720

QY 721 TTTTGGAGAAAAATCCAGAGTGGTGGATCTGAACTCTTAACAGAGGAGGTAAGATTATAC 780
Db 721 TTTTGGAGAAAAATCCAGAGTGGTGGATCTGAACTCTTAACAGAGGAGGTAAGATTATAC 780

QY 781 AGCTGCAACCTCTGTAACCTCTCAGTGTCCATTAAGGAGAACTAAAGAGAACCGATACC 840
Db 781 AGCTGCAACCTCTGTAACCTCTCAGTGTCCATTAAGGAGAACTAAAGAGAACCGATACC 840

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Db 841 ATTTTCTGGCCAGGTTCTCTCTGGTTAAACGCTGTGGTGGACTGTGCTGTGCTC 900
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Db 961 CTTTCAGTTGAGACCAAAAGACCGGTGTGAGGGGATTTGCACAAATCACTCACCAGAGTGCC 1020

QY 1021 CTGAGACCAATGAGGAGTGTGACTGTGTGTCAGAGGAGACACAGAGGATAGCCGAT 1080
Db 1021 CTGAGACCAATGAGGAGTGTGACTGTGTGTCAGAGGAGACACAGAGGATAGCCGAT 1080

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Db 1081 CACCACAGCAGCTCTTGGCCAGAGCTGTGAGTGTGAGTGTGCTTCAAGGACCTTTCATCTTCAGGA 1140

QY 1141 TATGCGTTATCTCCATCTTAATCTCAGTTGTTTGTCTTCAAGGACCTTTCATCTTCAGGA 1200
Db 1141 TATGCGTTATCTCCATCTTAATCTCAGTTGTTTGTCTTCAAGGACCTTTCATCTTCAGGA 1200

QY 1201 TTTTACAGTGCATTTCTGAAAGAGAGACATCAAAACAGAAATTAGGAGTTGTGCAACAGCTCT 1260
Db 1201 TTTTACAGTGCATTTCTGAAAGAGAGACATCAAAACAGAAATTAGGAGTTGTGCAACAGCTCT 1260

QY 1261 TTTTGAGAGGAGGCTTAAAGGACAGGAGAAAGGTCTTCAATCGTGGGAAAGAAATTAAT 1320
Db 1261 TTTTGAGAGGAGGCTTAAAGGACAGGAGAAAGGTCTTCAATCGTGGGAAAGAAATTAAT 1320

QY 1321 GTTGTATTAAATAGATCACCAGCTAGTTTTCAGAGTTTACCATGTACGTATTCCATCTAGCTG 1380
Db 1321 GTTGTATTAAATAGATCACCAGCTAGTTTTCAGAGTTTACCATGTACGTATTCCATCTAGCTG 1380

QY 1381 GGTTCTGTATTTCAGTTCTTTTCGATACGGCTTAGGGTAAATGTCAGTACAGAGAAATAACT 1440
Db 1381 GGTTCTGTATTTCAGTTCTTTTCGATACGGCTTAGGGTAAATGTCAGTACAGAGAAATAACT 1440

QY 1441 GTGCAAGTGTAGACCTGATTCGGTTCGCTTAACTCTAAAGCTCCATGTCTCTGGGCC 1500
Db 1441 GTGCAAGTGTAGACCTGATTCGGTTCGCTTAACTCTAAAGCTCCATGTCTCTGGGCC 1500

QY 1501 TAAAACTGATATAAAATCTGGATTTTTTTTTTTTTTTTGTCTCATATTTCACATATGTAAAC 1560
Db 1501 TAAAACTGATATAAAATCTGGATTTTTTTTTTTTTTTTGTCTCATATTTCACATATGTAAAC 1560

QY 1561 CAGAACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGAATTA 1620
Db 1561 CAGAACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGAATTA 1620

QY 1621 AACTTGTGTCRTGCTGTAGACAGACTGGATTTTTTTCATATTTTCTTATTAATAATTTCTGC 1680
Db 1621 AACTTGTGTCRTGCTGTAGACAGACTGGATTTTTTTCATATTTTCTTATTAATAATTTCTGC 1680

QY 1681 CATTTAGAAAGAGAGAACTACATTCATGTTTGGAGAGATTAACCTGAAAGAGAGTG 1740
Db 1681 CATTTAGAAAGAGAGAACTACATTCATGTTTGGAGAGATTAACCTGAAAGAGAGTG 1740

QY 1741 GCCTTATCTTCATCTTATCCATTAAGTCAGTTTATTTGTTTTCATTTGTGTACATTTTTTAT 1800
Db 1741 GCCTTATCTTCATCTTATCCATTAAGTCAGTTTATTTGTTTTCATTTGTGTACATTTTTTAT 1800

QY 1801 TCTCCTTTTTCACATTAATACTGTTGGCTTTTCTAACTCTGCTTAAATATATCTATTTTTTAC 1860
Db 1801 TCTCCTTTTTCACATTAATACTGTTGGCTTTTCTAACTCTGCTTAAATATATCTATTTTTTAC 1860

QY 1861 CAAAGGTATTATTAATTTCTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGTGTA 1920
Db 1861 CAAAGGTATTATTAATTTCTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGTGTA 1920

QY 1921 TTTTCTTAAACAACTTGTATATGACAGAGAAACAAAGATGGATATATAAATAATTTGTTC 1980
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QY 1981 CCTGGACAAAAATACATGATNTCCATCCCGGAATGGTCTAGAGTTGGATTAAACCTGC 2040
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QY 2041 ATTTTAAAAAACCCTGAATTTGGGAANGAANTTTGGTAAGTTGGCCCAANCTTTTGTGAAA 2100
DB |||||
2041 ATTTTAAAAAACCCTGAATTTGGGAANGAANTTTGGTAAGTTGGCCCAANCTTTTGTGAAA 2100
QY 2101 ATAATTAA 2108
DB |||||
2101 ATAATTAA 2108

RESULT 2

US-10-131-600-2
; Sequence 2, Application US/10131600
; Publication No. US20030082670A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/10/131,600
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/410,349
; FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/1108,109
; FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/110,749
; FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2108
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (2002)
; OTHER INFORMATION: can be a, c, g or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (2065)
; OTHER INFORMATION: can be a, c, g or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (2070)
; OTHER INFORMATION: can be a, c, g or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (2089)
; OTHER INFORMATION: can be a, c, g or t

US-10-131-600-2
Query Match 99.8%; Score 2103.6; DB 14; Length 2108;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCGCGGTGAGTCTCTACCCAGTCAGCAAAATGAGCCTCTTCGGGCTTCTCCTG 60
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QY 61 GTGACATCTGCCCTGGCCGGCCAGAGACGAGGACTCAGCGGGAATCCACCTGAGTAGT 120
DB |||||
61 GTGACATCTGCCCTGGCCGGCCAGAGACGAGGACTCAGCGGGAATCCACCTGAGTAGT 120
QY 121 AAAATTCAGTCTTCCAGCAACCAAGGAAACAGAACGAGAGTACAAGATCCTCAGCATGAGAGA 180
DB |||||
121 AAAATTCAGTCTTCCAGCAACCAAGGAAACAGAACGAGAGTACAAGATCCTCAGCATGAGAGA 180
QY 181 ATTATTACTGTCTACTAATCGAAGTATTCACAGCCCAAGGTTTCTCATACTTATCCA 240
DB |||||
181 ATTATTACTGTCTACTAATCGAAGTATTCACAGCCCAAGGTTTCTCATACTTATCCA 240
QY 241 AGAAATACGGTCTTGGTATGGAGATTAGTACAGTAGAGGAAAATGATGGATACAACTT 300
DB |||||
241 AGAAATACGGTCTTGGTATGGAGATTAGTACAGTAGAGGAAAATGATGGATACAACTT 300
QY 301 ACGTTTGTGAAAGATTTTGGGCTTGAAGACCCAGAAAGATGACATATGCAAGTATGATTTT 360
DB |||||
301 ACGTTTGTGAAAGATTTTGGGCTTGAAGACCCAGAAAGATGACATATGCAAGTATGATTTT 360
QY 361 GTAGAAAGTTGAGGAAACCCAGTCTATATATTAGGCGCTGGTGTCTGTGACT 420
DB |||||
361 GTAGAAAGTTGAGGAAACCCAGTCTATATATTAGGCGCTGGTGTCTGTGACT 420
QY 421 GTACAGGAAACACATTTCTAAAGGAATCAAAATAGGATAAGATTCTGATCTGATGA 480
DB |||||
421 GTACAGGAAACACATTTCTAAAGGAATCAAAATAGGATAAGATTCTGATCTGATGA 480
QY 481 TATTTTCTCTGAAACCAAGGTTCTGCATCCACTCAACATTTGTCTATGCCAATTCACA 540
DB |||||
481 TATTTTCTCTGAAACCAAGGTTCTGCATCCACTCAACATTTGTCTATGCCAATTCACA 540
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DB |||||
541 GAAGCTGTGAGTCTTCAAGTCTACCCCTTCCAGCTTTGCCACTGGACCTGCTTAATAAT 600
QY 601 GCTATAACTGCCCTTTAGTACCTTGGAGACCTTATTCGATATCTTGAACAGAGAGATGG 660
DB |||||
601 GCTATAACTGCCCTTTAGTACCTTGGAGACCTTATTCGATATCTTGAACAGAGAGATGG 660
QY 661 CAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTCTTTCGGCAAGGCTTTGTT 720
DB |||||
661 CAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTCTTTCGGCAAGGCTTTGTT 720
QY 721 TTTGGAAGAAAATCCAGAGTGGTGAATCTGAACCTTTCTAACAGAGAGGTTAAGATTATAC 780
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721 TTTGGAAGAAAATCCAGAGTGGTGAATCTGAACCTTTCTAACAGAGAGGTTAAGATTATAC 780
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DB |||||
781 AGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAACCGGATACC 840
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DB |||||
841 ATTTTCTGGCCAGGTTGTCTCTGTTTAAACCGTGTGGGAACTGTGCCCTGTGTCTC 900
QY 901 CACAATTCGAATGAATGTCTCCCAAGCAAGTTTACTTAAATAATACCACGAGGTC 960
DB |||||
901 CACAATTCGAATGAATGTCTCCCAAGCAAGTTTACTTAAATAATACCACGAGGTC 960
QY 961 CTTGAGTTGAGCAACCAAGACCGGTGTGAGGGGATTCACAATCTACTCACCACGCTGGCC 1020
DB |||||
961 CTTGAGTTGAGCAACCAAGACCGGTGTGAGGGGATTCACAATCTACTCACCACGCTGGCC 1020
QY 1021 CTGAGGACCATGAGGAGTGTGACTGTGTGTCAGAGGAGCACAAGGAGGATAGCCGAT 1080
DB |||||
1021 CTGAGGACCATGAGGAGTGTGACTGTGTGTCAGAGGAGCACAAGGAGGATAGCCGAT 1080
QY 1081 CACCACGAGAGCTCTTGGCCAGAGCTGTGCAGTGCTGCTGATTTCTATTAGAGAACG 1140

1081 CACCACAGCAGCTCTTGCCAGAGCTGTGCAGTGTGAGTCTATTAGAGACG 1140
1141 TATCGGTATCTCCATCTTATCTCAGTGTGTTGCTCAAGACCTTTCATCTCAGA 1200
1141 TATCGGTATCTCCATCTTATCTCAGTGTGTTGCTCAAGACCTTTCATCTCAGA 1200
1201 TTTACAGTGCATCTCTGAAGAGAGACATCAACAGAAATTAGAGTTGTGCAACGCTCT 1260
1201 TTTACAGTGCATCTCTGAAGAGAGACATCAACAGAAATTAGAGTTGTGCAACGCTCT 1260
1261 TTTGAGAGAGCCTTAAGGACAGAGAAAGCTTCTCAATCGTGGAAAGAAATTAAT 1320
1261 TTTGAGAGAGCCTTAAGGACAGAGAAAGCTTCTCAATCGTGGAAAGAAATTAAT 1320
1321 GTTGATTAAATAGATCACCGCTAGTTTCAGAGTTTACCATGTACGTATTCCACTAGCTG 1380
1321 GTTGATTAAATAGATCACCGCTAGTTTCAGAGTTTACCATGTACGTATTCCACTAGCTG 1380
1381 GGTTCGTATTTTCAGTCTTTTCGATACGGCTTAGGTAATGTACATATGTAAAC 1440
1381 GGTTCGTATTTTCAGTCTTTTCGATACGGCTTAGGTAATGTACATATGTAAAC 1440
1441 GTGCAAGTGCACCTGATTCGGTTCCTTAACTCTAAGCTCCATGTCTGGGCC 1500
1441 GTGCAAGTGCACCTGATTCGGTTCCTTAACTCTAAGCTCCATGTCTGGGCC 1500
1501 TAAATCGTATAAATCTCGATTTTCTGCTCATATTCATATGTAAAC 1560
1501 TAAATCGTATAAATCTCGATTTTCTGCTCATATTCATATGTAAAC 1560
1561 CAGAACATCTATGTACTACAACTGGTTTAAAGGAACATGTGCTATGAATTA 1620
1561 CAGAACATCTATGTACTACAACTGGTTTAAAGGAACATGTGCTATGAATTA 1620
1621 AACTGTGTCGTGATAGGACAGACTGGATTTTTCATATTTCTTAAATTTCTGC 1680
1621 AACTGTGTCGTGATAGGACAGACTGGATTTTTCATATTTCTTAAATTTCTGC 1680
1681 CATTTAGAGAGAGAACTACATTTTCATGTTTGGAGAGATAAACCCTGAAAGAGAGTG 1740
1681 CATTTAGAGAGAGAACTACATTTTCATGTTTGGAGAGATAAACCCTGAAAGAGAGTG 1740
1741 GCCTATCTCTTATCGATAAGTCACTTATTTGTTTCACTATGTTTATAT 1800
1741 GCCTATCTCTTATCGATAAGTCACTTATTTGTTTCACTATGTTTATAT 1800
1801 TCTCCCTTTGACATTAATCTGTTGGCTTTCTCAATCTGTTAAATATATCTTTTAC 1860
1801 TCTCCCTTTGACATTAATCTGTTGGCTTTCTCAATCTGTTAAATATATCTTTTAC 1860
1861 CAAAGTATTTAATCTCTTTTATGCAACTTAGATCAACTATTTTGTGTTGTTGTTG 1920
1861 CAAAGTATTTAATCTCTTTTATGCAACTTAGATCAACTATTTTGTGTTGTTGTTG 1920
1921 TTTTCTTAAACAAATGTTATAGCCAGAGGACAAAGATGATATATAAATATTGTC 1980
1921 TTTTCTTAAACAAATGTTATAGCCAGAGGACAAAGATGATATATAAATATTGTC 1980
1981 CTTGGACAAAATACATGATATNTCCATCCCGGAATGCTGCTAGAGTTGATTAACCTGC 2040
1981 CTTGGACAAAATACATGATATNTCCATCCCGGAATGCTGCTAGAGTTGATTAACCTGC 2040
2041 ATTTTAAACAACTGAATGGGAAGGAANTTGGTAAGGTTGGCCAAANCTTTTTGAAA 2100
2041 ATTTTAAACAACTGAATGGGAAGGAANTTGGTAAGGTTGGCCAAANCTTTTTGAAA 2100
2101 ATAATTA 2108
2101 ATAATTA 2108

US-10-178-442-1
; Sequence 1, Application US/10178442
; Publication No. US20030113870A1
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
; FILE REFERENCE: 11669.112USD2
; CURRENT APPLICATION NUMBER: US/10/178,442
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 09/265,686
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: US 09/184,216
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: US 09/040,220
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2825
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2689)..(2689)
; OTHER INFORMATION: Any nucleotide
US-10-178-442-1

Query Match 93.9%; Score 1979.4; DB 14; Length 2825;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

QY 2 CCGCGCGTGAGTGAGCTCTCACCCAGTCAGCCCAATAGAGCTCTTCGGGCTTCTCCTGG 61
DB 224 CCGCGCGTGAGTGAGCTCTCACCCAGTCAGCCCAATAGAGCTCTTCGGGCTTCTCCTGC 293
QY 62 TCACATCTGCCCTGCGCGCCAGAGACGAGGAGCTCAGCGGGAATCCAACTGAGTAGTA 121
DB 284 TCACATCTGCCCTGCGCGCCAGAGACGAGGAGCTCAGCGGGAATCCAACTGAGTAGTA 343
QY 122 AATTCAGTTTTCAGACACAGGACAGACGAGTACAAGTCTTCAGCATGAGAGAA 181
DB 344 AATTCAGTTTTCAGACACAGGACAGACGAGTACAAGTCTTCAGCATGAGAGAA 403
QY 182 TTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGTTTCTCTCATCTTATCCAA 241
DB 404 TTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGTTTCTCTCATCTTATCCAA 463
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;; PRIOR APPLICATION NUMBER: 09/514,010
;; PRIOR FILING DATE: 2000-02-25
;; PRIOR APPLICATION NUMBER: 09/516,745
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: 09/572,002
;; PRIOR FILING DATE: 2000-05-14
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;; PRIOR FILING DATE: 2000-06-19
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;; PRIOR FILING DATE: 2000-09-30
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;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (288)...(1322)
US-09-796-753-5

Query Match 93.9%; Score 1979.4; DB 11; Length 2839;
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Db 2342 TAATTAA 2348

RESULT 5

US-09-978-295A-487
; Sequence 487, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250

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; PRIOR APPLICATION NUMBER: 60/085697
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Query Match 93.9%; Score 1979.4; DB 10; Length 2849;
Best Local Similarity 97.7%; Pred. No. 0;
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QY 1622 ACTTGTCGTCGTGATAGGACAGATGGAATTTTTCATATTTCTATTAAATTTCTGCC 1681
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Db 1930 ATTTAGAAGAGAACTACATTCATGTTTTCGAGAGATAAACCCTGAAAGAGAGTGG 1989
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RESULT 6

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; Sequence 487, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
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; APPLICANT: Hillan, Kenneth J.
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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RESULT 7

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; Sequence 487, Application US/09978192A

; Patent No. US20020177553A1

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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C9

; CURRENT APPLICATION NUMBER: US/09/978,192A

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 93.9%; Score 1979.4; DB 10; Length 2849;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;
QY 2 CCCGCGTGAGTGAGCTCTCACCCGAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCTGG 61
Db 250 CCCGCGTGAGTGAGCTCTCACCCGAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCTGC 309
QY 62 TGACATCTGCCCTGGCGGCCAGAGACGAGGACTCAGGCGGAATCCAACTGAGTAGTA 121

Db 310 TCACATCTGCCCTGGCGGCCAGAGACAGGGACTCAGGCGGAATCCAACTGAGTAGTA 369
QY 122 AATTCAGTTTTTCCAGACAACAGGAACAGAAACGAGTCAAGATCTCTCAGCATGAGAGAA 181
Db 370 AATTCAGTTTTTCCAGACAACAGGAACAGAAACGAGTCAAGATCTCTCAGCATGAGAGAA 459
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QY 242 GNAATACGGTCTTGTGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATAACAATTA 301
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Db 550 CGTTTGAATGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTG 609
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Best Local Similarity 97.7%; Pred. No. 0;
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Db 250 CCGCGGTGAGTGAGCTCTCACCCAGTCAGCCCAATAGCCTCTTCGGGCTTCTCTGG 309
QY 62 TGACATCTGCCCTGGCCGCGGAGACGAGGAGGAGTCAAGATCTCTCAGCATGAGTAA 121
Db 310 TGACATCTGCCCTGGCCGCGGAGACGAGGAGGAGTCAAGATCTCTCAGCATGAGTAA 369
QY 122 AATTCAGTTTCCAGCAACAGGAAACAGACGAGGAGTCAAGATCTCTCAGCATGAGTAA 181
Db 370 AATTCAGTTTCCAGCAACAGGAAACAGACGAGGAGTCAAGATCTCTCAGCATGAGTAA 429
QY 182 TTATTACTGTGTACTAATGAAGTATTACAGCCCAAGGTTTCTCTACTATCTATCCAA 241
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QY 242 GAATACGGTCTTGGTATGGAGATTAGTAGGAGTAAATGTATGGATCAACTTA 301

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
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PRIOR FILING DATE: 2001-07-30
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Query Match 93.9%; Score 1979.4; DB 11; Length 2849;
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QY 1862 AAAGGTATTTAATATCTTTTATGACAACTTAGATCAACTATTTTATGCTTGTAAAT 1921
Db 2110 AAAGGTATTTAATATCTTTTATGACAACTTAGATCAACTATTTTATGCTTGTAAAT 2169
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Db 2170 TTTTCTAAACAAATGTTATAGCCAGAGAAACAAAGATG---ATATAAATAATGTTGCC 2226
QY 1982 CTGGACAAAATACATGATATNTCCATCCCGGAATGCTAGAGTTGGATTAAACCTGCA 2041
Db 2227 TCTGACAAAATACATGATATNT---CATCTCGATGTTGCTAGAGTTAGATT---AATCTGCA 2284
QY 2042 TTTTAAAAACCTGAATTTGGGAANGAANTTGGTAAGTGTGGCCAAANCTTTTTTGAAA 2101
Db 2285 TTTTAAAAACCTGAATTT---GGATAGAAATGTTGAAGTT---GCAAGACTTTTGAAA 2338
QY 2102 TAATTAA 2108
Db 2339 TAATTAA 2345
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US-09-978-608A-487
; Sequence 487, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 487
; LENGTH: 2849
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2715
; OTHER INFORMATION: unknown base
US-09-978-608A-487
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Query Match 93.9%; Score 1979.4; DB 11; Length 2849;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

QY 2 CCGCGCGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGG 61
Db 250 CCGCGCGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGG 309
QY 62 TGACATCTGCCCTGGCCGCGCAGAGACGAGGGAACCTCAGCGGAAATCCAACTGAGTAGTA 121
Db 310 TGACATCTGCCCTGGCCGCGCAGAGACGAGGGAACCTCAGCGGAAATCCAACTGAGTAGTA 369
QY 122 AATTCAGTTTCCAGCAGCAGGAGACAGAAAGGAGTCAAGATCTCTCAGCATGAGAGAA 181
Db 370 AATTCAGTTTCCAGCAGCAGGAGACAGAAAGGAGTCAAGATCTCTCAGCATGAGAGAA 429
QY 182 TTATTACTCTGTCTACTAATGGAAGTATTACAGGCCAAAGTTTCTCTACTACTTATCCAA 241
Db 430 TTATTACTCTGTCTACTAATGGAAGTATTACAGGCCAAAGTTTCTCTACTACTTATCCAA 489
QY 242 GAAATACCGTCTTGGTATGAGAGATTAGTAGCAGTAGAGAGAAATGTATGATACAACTTA 301
Db 490 GAAATACCGTCTTGGTATGAGAGATTAGTAGCAGTAGAGAGAAATGTATGATACAACTTA 549
QY 302 CGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTG 361
Db 550 CGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTTG 609
QY 362 TAGAAGTTGAGAAACCCAGTGTAGAACTATATTAGGCGCTGCTGTTCTGGTACTG 421
Db 610 TAGAAGTTGAGAAACCCAGTGTAGAACTATATTAGGCGCTGCTGTTCTGGTACTG 669
QY 422 TACCAGGAAAACAGATTTCTTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGTGAAT 481
Db 670 TACCAGGAAAACAGATTTCTTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGTGAAT 729
QY 482 ATTTTCTCTCTGACACAGGTTCTGCATCCACTAGCAACATTGTCTAGCCACATTTACAG 541
Db 730 ATTTTCTCTCTGACACAGGTTCTGCATCCACTAGCAACATTGTCTAGCCACATTTACAG 789
QY 542 AAGCTGTGAGTCTCTCAGTGTCTACCCCTTACGCTTTGCCACTTGGACCTGCTCTTAATAATG 601
Db 790 AAGCTGTGAGTCTCTCAGTGTCTACCCCTTACGCTTTGCCACTTGGACCTGCTCTTAATAATG 849
QY 602 CTATAACTGCCCTTTAGTACCTTTGGAGACCTTATTCGATATCTTTGAAACCCAGAGATGGC 661
Db 850 CTATAACTGCCCTTTAGTACCTTTGGAGACCTTATTCGATATCTTTGAAACCCAGAGATGGC 909
QY 662 AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTCTTGGCAAGGCTTTTGT 721
Db 910 AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTCTTGGCAAGGCTTTTGT 969
QY 722 TTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGAGGTAAGATTATACA 781
Db 970 TTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGAGGTAAGATTATACA 1029
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782 GCTGCACACCTCGTAACCTCTCAGTGTCCATAGGGAAGAACTAAGAGAACCGATACCA 841
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1030 GCTGCACACCTCGTAACCTCTCAGTGTCCATAGGGAAGAACTAAGAGAACCGATACCA 1089
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842 TTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTGGTGGGAACTGTGCTGTGTCTCC 901
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1090 TTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTGGTGGGAACTGTGCTGTGTCTCC 1149
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902 ACAATTCGAATCAATGCTCAATGCTCCCAAGCAAAAGTTACTAAAATAACCAAGGCTCC 961
Db
1150 ACAATTCGAATCAATGCTCAATGCTCCCAAGCAAAAGTTACTAAAATAACCAAGGCTCC 1209
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962 TTCAGTTGAGACCAAGACCGGTGTGACGGGATGTCACAAATCACTCACCGACGTGGCCC 1021
Db
1210 TTCAGTTGAGACCAAGACCGGTGTGACGGGATGTCACAAATCACTCACCGACGTGGCCC 1269
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1022 TGGAGCACCATGAGGAGTGTACTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGCATC 1081
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1270 TGGAGCACCATGAGGAGTGTACTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGCATC 1329
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1082 ACCACAGCAGCTCTTGGCCAGAGCTGTGCAGTGCAGTGGCTGATTTCTATTAGAGAACGT 1141
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1330 ACCACAGCAGCTCTTGGCCAGAGCTGTGCAGTGCAGTGGCTGATTTCTATTAGAGAACGT 1389
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1142 ATGCGTTATCTCAATCCTTAATCTCAGTTGTTTGGTTCAAGGACCTTTCACTTCCAGGAT 1201
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1390 ATGCGTTATCTCAATCCTTAATCTCAGTTGTTTGGTTCAAGGACCTTTCACTTCCAGGAT 1449
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1202 TTACATGTCATTTCTGAAGAGGAGACATCAACAGAAATTAGGATTTGTCACAGCTCTT 1261
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1450 TTACATGTCATTTCTGAAGAGGAGACATCAACAGAAATTAGGATTTGTCACAGCTCTT 1509
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1262 TTGAGAGGAGGCTTAAGAGACAGGAGAAAGGCTTCAATCGTGGAAAGAAATTAATG 1321
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1510 TTGAGAGGAGGCTTAAGAGACAGGAGAAAGGCTTCAATCGTGGAAAGAAATTAATG 1569
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1322 TTGATTAATAAGATCAACAGCTAGTTTTCAGATTAACATGATACGTTATCCACTAGCTGG 1381
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1562 AGAATCTTCTATCTACTACAAACCTGGTTTAAAAAGGAACTATGTTGCTATGAATTA 1621
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1810 AGAATCTTCTATCTACTACAAACCTGGTTTAAAAAGGAACTATGTTGCTATGAATTA 1869
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1622 ACTTGTGCTGTGTAGACAGCTGGATTTTTCATATTTCTTATTAATAATTTCTGCC 1681
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1870 ACTTGTGCTGTGTAGACAGCTGGATTTTTCATATTTCTTATTAATAATTTCTGCC 1929
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1682 ATTTAGAGAGAGAACTCATTCATGTTTGGAGAGATAAACCTGAAAGAGAGTGG 1741
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1930 ATTTAGAGAGAGAACTCATTCATGTTTGGAGAGATAAACCTGAAAGAGAGTGG 1989
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1742 CCTTATCTTCTATCTGTAAGTCACTGTTTATTTGTTTTCATGTTGATATTTTATTT 1801
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1990 CCTTATCTTCTATCTGTAAGTCACTGTTTATTTGTTTTCATGTTGATATTTTATTT 2049
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1802 CTCCTTTTGAATATAAATCTGTTGGCTTTTCTAATCTTGTGTAATAATATCTATTTTACC 1861
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1862 AAAGGTATTTAATATCTTTTATGACAACTTAGATCAACTATTTTAGCTGGTAAAT 1921

Db 2110 AAAGGTATTTAATATCTTTTATGACAACTTAGATCAACTATTTTAGCTGGTAAAT 2169
Qy 1922 TTTTCTTAAACACAATTTTATAGCCAGAGGAACAAAGATGGATATAAAAAATTTGTGCC 1981
Db 2170 TTTTCTTAAACACAATTTTATAGCCAGAGGAACAAAGATG---ATATAAAATTTGTGC 2226
Qy 1982 CTGGACAAAATAACATGATATNTCCATCCCGGAATGCTGCTAGAGTTGGATTAAACCTGCA 2041
Db 2227 TCTGACAAAATAACATGATATTT-CATTCTCGTATGCTGCTAGAGTTAGATT-AATCTGCA 2284
Qy 2042 TTTTAAAAAACCTGATTTGGGAANGAANTTGGTAAGGTTGGCCAAANCTTTTTCGAAA 2101
Db 2285 TTTTAAAAAACCTGAAATTT---GGAATAGATTTGGTAAGTT---GCAAGAACTTTTTCGAAA 2338
Qy 2102 TAATTAA 2108
Db 2339 TAATTAA 2345

RESULT 11

US-09-978-585A-487
; Sequence 487, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 487
; LENGTH: 2849
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2715
; OTHER INFORMATION: unknown base
; US-09-978-585A-487

Query Match 93.9%; Score 1979.4; DB 11; Length 2849;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

QY 2 CCGCCGCTGAGTGTCTCACCCAGTCAGCAAAATGAGCCTCTTCGGGCTTCTCTGG 61
Db 250 CCGCCGCTGAGTGTCTCACCCAGTCAGCAAAATGAGCCTCTTCGGGCTTCTCTGG 309
QY 62 TGACATCTGCGCTGCGCCGAGAGACGAGGACCTCAGCGGAAATCCAACTGAGTAGTA 121
Db 310 TGACATCTGCGCTGCGCCGAGAGACGAGGACCTCAGCGGAAATCCAACTGAGTAGTA 369
QY 122 AATTCCAGTTTTCAGCAACCAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAA 181
Db 370 AATTCCAGTTTTCAGCAACCAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAA 429
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Db 430 TTATTACTGTGTACTAATGAAGTATTCACAGCCCAAGTTTCTCATACTTATCCAA 489
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Db 490 GAAATACCGTCTTGATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAACTTA 549
QY 302 CGTTTGATGAAGATTTGGGCTTGAAGACCCAGAAAGTACATATGCAAGTATGATTTTG 361
Db 550 CGTTTGATGAAGATTTGGGCTTGAAGACCCAGAAAGTACATATGCAAGTATGATTTTG 609
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Db 610 TAGAAGTTGAGAAACCCAGTGTATGAACTATATATTAGGGCGCTGGTGTCTGGTACTG 669
QY 422 TACCAGGAAACAGATTTCTAAGGAATCAAAATTAGGATAAGATTGTATCTGATGAT 481
Db 670 TACCAGGAAACAGATTTCTAAGGAATCAAAATTAGGATAAGATTGTATCTGATGAT 729
QY 482 ATTTTCTCTTGAACACAGGTTTCTGCATCCACTACAACATTTGTCATGCCACAATTCACAG 541
Db 730 ATTTTCTCTTGAACACAGGTTTCTGCATCCACTACAACATTTGTCATGCCACAATTCACAG 789
QY 542 AAGCTGTGAGTCTTCAGTGTCTACCCCTTACGCTTGGCTTGGCACTGAGACCTGCTTAATATG 601
Db 790 AAGCTGTGAGTCTTCAGTGTCTACCCCTTACGCTTGGCACTGAGACCTGCTTAATATG 849
QY 602 CTATACTGCCTTTAGTACTTGGAGACCTTATTGATATCTTGAACCCAGAGAGATGCG 661
Db 850 CTATACTGCCTTTAGTACTTGGAGACCTTATTGATATCTTGAACCCAGAGAGATGCG 909
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Db 910 AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTT 969
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Db 1030 GCTGCACACCTCGTAACCTTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACCGATACCA 1089
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QY 1022 TGGAGCACCATGAGGAGTGTGACTGTGTGTGAGAGGGAGCACAGGAGGATAGCCGATC 1081
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Db 1330 ACCACGAGAGCTCTTGCCAGAGCTGTGCACTGCACTGGCTGATTTCTATTAGAGAACGT 1389
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Db 1390 ATGCGTTATCTCATCTTAATCTCAGTTGTTTCTCAAGGACCTTTTCATCTTCAGGAT 1449
QY 1202 TTACAGTGCATTTCTGAAGAGAGACATCAAA CAGAATTTAGGAGTTGTCAACAGCTCTT 1261
Db 1450 TTACAGTGCATTTCTGAAGAGAGACATCAAA CAGAATTTAGGAGTTGTCAACAGCTCTT 1509
QY 1262 TTGAGAGAGGCTTAAAGACAGGAGAAAGGCTTCAATCTGTGGAGAAATTTAAATG 1321
Db 1510 TTGAGAGAGGCTTAAAGACAGGAGAAAGGCTTCAATCTGTGGAGAAATTTAAATG 1569
QY 1322 TTGTATTAAATAGATCACCGACTAGTTTCAGAGTTACCATGTACGTATTCCTACCTG 1381
Db 1570 TTGTATTAAATAGATCACCGACTAGTTTCAGAGTTACCATGTACGTATTCCTACCTG 1629
QY 1382 GTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAAATGTTCAGTACAGGAAAAAATG 1441
Db 1630 GTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAAATGTTCAGTACAGGAAAAAATG 1689
QY 1442 TGCAGTGTGAGACCTGATTCGGTTGCTTAACTCTAAAGCTCCATGTCTGGGCT 1501
Db 1690 TGCAGTGTGAGACCTGATTCGGTTGCTTAACTCTCTAAAGCTCCATGTCTGGGCT 1749
QY 1502 AAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGTAACC 1561
Db 1750 AAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGTAACC 1809
QY 1562 AGAACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACCTATGTCTATGAATTA 1621
Db 1810 AGAACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACCTATGTCTATGAATTA 1869
QY 1622 ACTGTGTCGTCTGATFAGGACAGACTGGATTTTTCATATTTCTTATTTAAATTTCTGCC 1681
Db 1870 ACTGTGTCGTCTGATFAGGACAGACTGGATTTTTCATATTTCTTATTTAAATTTCTGCC 1929
QY 1682 ATTTAGAGAGAGAACTACATTCATGTTTGGAGAGATAAACCTGGAAGAGAGTGG 1741
Db 1930 ATTTAGAGAGAGAACTACATTCATGTTTGGAGAGATAAACCTGGAAGAGAGTGG 1989
QY 1742 CTTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTTCATTTGTGTACATTTTATAT 1801
Db 1990 CTTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTTCATTTGTGTACATTTTATAT 2049
QY 1802 CTCTCTTTTGACATTAATCTGTTGGCTTTTCTAACTCTGTTAAATATATCTATTTTACC 1861
Db 2050 CTCTCTTTTGACATTAATCTGTTGGCTTTTCTAACTCTGTTAAATATATCTATTTTACC 2109
QY 1862 AAAGGTATTATAATTTCTTTTATGACAACTTAGATCAACTATTTTATAGCTTGGTAAAT 1921
Db 2110 AAAGGTATTATAATTTCTTTTATGACAACTTAGATCAACTATTTTATAGCTTGGTAAAT 2169
QY 1922 TTTTCTAAACAAATTTATAGCCAGAGGAA CAAAGATGGATATAAAATATTTGTGCC 1981
Db 2170 TTTTCTAAACAAATTTATAGCCAGAGGAA CAAAGATG---ATATAAATATTTGTGC 2226
QY 1982 CTGGACAAATAATACATGTATNTCCATCCCGAATGGTGTAGAGTTGGATTTAAACCTGCA 2041
Db 2227 TCTGCAAAATAATACATGTATTTT-CATTTCTGTATGGTGTAGAGTTAGATT-AACTGCA 2284
QY 2042 TTTTAAAAAACCTGAAATTTGGGAAGGAATTTGTAAGGTGGCCAAANCTTTTGTGAAA 2101
Db 2285 TTTTAAAAAACCTGAAATTT---GGATAGAAATTTGTAAGTT---GCAAGAGCTTTTGTGAAA 2338
QY 2102 TAAATTA 2108
Db 2339 TAAATTA 2345

RESULT 12

US-09-978-191A-487
; Sequence 487, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
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Query Match      93.9%; Score 1979.4; DB 11; Length 2849;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

Qy      2  CCCCCCGTGTAGTGTCTCTACCCCGAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCTGG 61
Db      250  CCCCCCGTGTAGTGTCTCTACCCCGAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCTGC 309

Qy      62  TGACATCTGCCCTGGCGGCGCAGAGACGAGGACTCTCAGCGGAATCCAACTGTAGTAGTA 121
Db      310  TGACATCTGCCCTGGCGGCGCAGAGACGAGGGAATCCAACTGTAGTAGTA 369

Qy      122  AATTCAGTCTTCCAGACAAAGGACAGACGAGGTACAGATCCTCAGCATGAGAA 181
Db      370  AATTCAGTCTTCCAGACAAAGGACAGACGAGGTACAGATCCTCAGCATGAGAA 429

Qy      182  TTATTACTGTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCTCATCTTATCCAA 241
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Db      430  TTATTACTGTCTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCTCATCTTATCCAA 489
Qy      242  GAAATACCGTCTTGTGTATGGAGATTAGTAGCAGTAGAGAAAATGTATGGATACAACCTTA 301
Db      490  GAAATACCGTCTTGTGTATGGAGATTAGTAGCAGTAGAGAAAATGTATGGATACAACCTTA 549
Qy      302  CGTTTGTATGAAAGATTTTGGGCTTGAAGACCCAGAAAGATGACATATGCAAGTAGATTTTG 361
Db      550  CGTTTGTATGAAAGATTTTGGGCTTGAAGACCCAGAAAGATGACATATGCAAGTAGATTTTG 609
Qy      362  TAGAAGTTGAGNACCCAGTGTGAACTATATATAGGCGCTGTGTGGTTCTGCTACTG 421
Db      610  TAGAAGTTGAGNACCCAGTGTGAACTATATATAGGCGCTGTGTGGTTCTGCTACTG 669
Qy      422  TACCAGGAAAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTGTATCTGATGAAT 481
Db      670  TACCAGGAAAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTGTATCTGATGAAT 729
Qy      482  ATTTTCTCTTGAACACAGGGTTCTGCATCCACTACAACATTGTCTATGCCACAAATCACAG 541
Db      730  ATTTTCTCTTGAACACAGGGTTCTGCATCCACTACAACATTGTCTATGCCACAAATCACAG 789
Qy      542  AAGCTGTGAGTCCCTTCAGTGTCTACCCCTTCAGCTTTCAGCTTTCGCACTGCACTTAATG 601
Db      790  AAGCTGTGAGTCCCTTCAGTGTCTACCCCTTCAGCTTTCGCACTGCACTTGAATTAATG 849
Qy      602  CTATAACTGCTCTTAGTACCTTGAAGACCTTTATTGATATCTTCAACCCAGAGAGATGCG 661
Db      850  CTATAACTGCTCTTAGTACCTTGAAGACCTTTATTGATATCTTGAACCCAGAGAGATGCG 909
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Db      910  AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGT 969
Qy      722  TTGGAAGAAATCCAGAGTGTGGATCTGAACCTTCTAACAGAGAGAGTAAATATACA 781
Db      970  TTGGAAGAAATCCAGAGTGTGGATCTGAACCTTCTAACAGAGAGAGTAAATATACA 1029
Qy      782  GCTGCACACCTCGTAACTTCTCAGTGTCTCAATAGGGAAGAACTAAAGAGAACCGATACCA 841
Db      1030  GCTGCACACCTCGTAACTTCTCAGTGTCTCAATAGGGAAGAACTAAAGAGAACCGATACCA 1089
Qy      842  TTTTCTGGCCAGGTTGTCTCTCTGTTAAACCGCTGTGGTGGGAACCTGTCTGTCTCC 901
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Db      1270  TGGAGACCATGAGAGAGTGTGACTGTGTGTGAGGAGGAGACAGAGATAGCCGATC 1329
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Db      1330  ACCACGAGCAGCTCTTCCCGAGAGCTGTGCACTGAGTGGCTGATTCTTATTAGAGAACT 1389
Qy      1142  ATGCGTTTATCTCCATCTTAACTCAGTTGTTTCTTCAAGGACCTTTCATCTTCAGGAT 1201
Db      1390  ATGCGTTTATCTCCATCTTAACTCAGTTGTTTCTTCAAGGACCTTTCATCTTCAGGAT 1449
Qy      1202  TTACAGTGCATTTGAAAGAGGAGACATCAAAAGAAATTAGAGTTGTGCAACAGCTCTT 1261
Db      1450  TTACAGTGCATTTGAAAGAGGAGACATCAAAAGAAATTAGAGTTGTGCAACAGCTCTT 1509
Qy      1262  TTGAGAGAGGCGCTTAAAGGACAGAGAAAGGTTCTTCAATCGTGAAGAAATTAATG 1321
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Qy 1562 AGAATCTCTATGTAACAACTGGTTTTTAAAAAGGAACATATGTTGCTATGAATTA 1621
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Qy 1622 ACTTGTCTGCTGCTGATGAGGACAGCTGATTTTTCATATTTCTTATTAATAATTTCTGCC 1681
Db 1870 ACTTGTCTGCTGCTGATGAGGACAGCTGATTTTTCATATTTCTTATTAATAATTTCTGCC 1929
Qy 1682 ATTTAGAGAGAGAACTACATTCATGTTTGGAGAGATAAACTGAAAAAGAGAGTGG 1741
Db 1930 ATTTAGAGAGAGAACTACATTCATGTTTGGAGAGATAAACTGAAAAAGAGAGTGG 1989
Qy 1742 CCTTATCTTCACTTATCGATAAGTCAGTTTATTTGTTTCATTTGTTGATACATTTTATATT 1801
Db 1990 CCTTATCTTCACTTATCGATAAGTCAGTTTATTTGTTTCATTTGTTGATACATTTTATATT 2049
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Db 2050 CTCCTTTTGACATTAATCTGTTGCTTTTCTTAATCTTGTTAAATATATCTATTTTACC 2109
Qy 1862 AAAGGTATTTAATATCTTTTTTATGCAACTAGATCAACTATTTTTAGCTTGGTAAAT 1921
Db 2110 AAAGGTATTTAATATCTTTTTTATGCAACTAGATCAACTATTTTTAGCTTGGTAAAT 2169
Qy 1922 TTTTCTAAACAATTTGTTATAGCCAGAGAACAAAGATGATATAAAATATTTGTTGCC 1981
Db 2170 TTTTCTAAACAATTTGTTATAGCCAGAGAACAAAGATG---ATATAAAATATTTGTTGC 2226
Qy 1982 CTGACAAAAATACATGTATNTCCATCCGGAATGGTGTAGAGTTGGATTAAACCTGCA 2041
Db 2227 TCTGACAAAAATACATGTATTT-CAATCTCGTATGGTGTAGAGTTAGATT-AACTGCA 2284
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Qy 2102 TAATTA 2108
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; Publication No. US20030050240A1
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Peoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Query Match 93.9%; Score 1979.4; DB 11; Length 2849;

Best Local Similarity 97.7%; Pred. No. 0;

Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

Qy 2 CCGCGGTGAGTGAGCTCTCACCCNAGTCAGCCGAATGAGCCTTTGGGGCTTCTCTGG 61

Db 250 CCGCGGTGAGTGAGCTCTCACCCNAGTCAGCCGAATGAGCCTTTGGGGCTTCTCTGG 309

Qy 62 TGACATCTGCCCTGGCGGCCAGAGACGAGGAGTTCAGCGGGAATCCAACTCAGTAGTA 121

Db 310 TGACATCTGCCCTGGCGGCCAGAGACGAGGAGTTCAGCGGGAATCCAACTCAGTAGTA 369

Qy 122 AATTCAGTTTTCCAGCAACAAGGAAACAGAACGGAGTCAAGATCTCTCAGCATGAGAGAA 181

Db 370 AATTCAGTTTTCCAGCAACAAGGAAACAGAACGGAGTCAAGATCTCTCAGCATGAGAGAA 429

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Qy 242 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATCAACTTA 301

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Qy 302 CGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTG 361

Db 550 CGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTTG 609

Qy 362 TAGAAGTTGAGGAACCCAGTGTGAACATATATTAGGGCGCTGGTGTCTTGGTACTG 421

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Qy 422 TACCAGGAAAACAGATTTCTAAGGAAATCAATTAGGATAGATTTGTATCTGATGAT 481
Db 670 TACCAGGAAAACAGATTTCTAAGGAAATCAATTAGGATAGATTTGTATCTGATGAT 729
Qy 482 ATTTTCTCTTCTGAACACAGGGTCTGTCATCCATACAAACATTTGTCAGCCCAACATTCACAG 541
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Qy 1262 TTCAGAGGAGGCTTAAAGGACAGGAAAAGGCTTCAATCGTGGAAAAGAAAATTAATG 1321
Db 1510 TTCAGAGGAGGCTTAAAGGACAGGAAAAGGCTTCAATCGTGGAAAAGAAAATTAATG 1569
Qy 1322 TTGTATTAATATAGATACACAGCTAGTTTTCAGATTTACCATGTCATTCACATAGCTGG 1381
Db 1570 TTGTATTAATATAGATACACAGCTAGTTTTCAGATTTACCATGTCATTCACATAGCTGG 1629
Qy 1382 GTTCTGTATTTCTAGTCTTTTCGATACGGCTTAGGTAATCTCAGTACAGGAAAACCTG 1441
Db 1630 GTTCTGTATTTCTAGTCTTTTCGATACGGCTTAGGTAATCTCAGTACAGGAAAACCTG 1689
Qy 1442 TGCAAGTGACACCTGATTCGGTTCCTTGCCTTAACTCTTAAAGCTCCATGTCCTGGCCCT 1501
Db 1690 TGCAAGTGACACCTGATTCGGTTCCTTGCCTTAACTCTTAAAGCTCCATGTCCTGGCCCT 1749

Qy 1502 AAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGTAACC 1561
Db 1750 AAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGTAACC 1809
Qy 1562 AGAATCTTCTATGTACTACAAACCTGGTTTTTAAAAGAACTATGTTGCTATGAATTA 1621
Db 1810 AGAATCTTCTATGTACTACAAACCTGGTTTTTAAAAGAACTATGTTGCTATGAATTA 1869
Qy 1622 ACTGTGTCCTCTGATAGGACAGACTGGATTTTTTTCATATTTCTTAAATTTCTCTGCC 1681
Db 1870 ACTGTGTCCTCTGATAGGACAGACTGGATTTTTTTCATATTTCTTAAATTTCTCTGCC 1929
Qy 1682 ATTTAGAAGAGAGAACTACATTTTCATGTTTGGAGAGATAAACTGAAAGAGAGTGG 1741
Db 1930 ATTTAGAAGAGAGAACTACATTTTCATGTTTGGAGAGATAAACTGAAAGAGAGTGG 1989
Qy 1742 CTTATCTTTCATCTTATCGATTAAGTCAGTTTATTTGTTTCATTTGCTGATATTTTATTT 1801
Db 1990 CTTATCTTTCATCTTATCGATTAAGTCAGTTTATTTGTTTCATTTGCTGATATTTTATTT 2049
Qy 1802 CTCCTTTGACATTAACCTGTTGGCTTTTCTAATCTTGTAAATATATCTATTTTATACC 1861
Db 2050 CTCCTTTGACATTAACCTGTTGGCTTTTCTAATCTTGTAAATATATCTATTTTATACC 2109
Qy 1862 AAAGGTATTTAAATATTTCTTTTTTATGACAACTTAGATCAACTATTTTATAGCTTGGTAAAT 1921
Db 2110 AAAGGTATTTAAATATTTCTTTTTTATGACAACTTAGATCAACTATTTTATAGCTTGGTAAAT 2169
Qy 1922 TTTTCTAAACACAAATTTATAGCCAGAGAACAAAGATGGATATAAAATATTTGTTGCC 1981
Db 2170 TTTTCTAAACACAAATTTATAGCCAGAGAACAAAGATG---ATATAAATATTTGTTGCC 2226
Qy 1982 CTGACAAAATACATGATNTCCATCCCGAATGCTGTAGAGTTGGATTAACCTGCA 2041
Db 2227 TCTGACAAAATACATGATNTT---CATCTCGATGCTGTAGAGTTAGATTT---AATCTGCA 2284
Qy 2042 TTTTAAAAAACCTGAAATTTGGGAAGGAANTTGTAAAGTTGGCCCAANCTTTTGTGAAAA 2101
Db 2285 TTTTAAAAAACCTGAAATTT---GGAATAGAAATTTGTAAGTT---GCAAGAGACTTTTGTGAAAA 2338
Qy 2102 TAATTA 2108
Db 2339 TAATTA 2345

RESULT 14
US-09-978-564A-487
; Sequence 487, Application US/09978564A
; Publication No. US2003050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kiljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C25
CURRENT FILING DATE: 2001-10-16
PRIORITY APPLICATION NUMBER: US/09/978,564A
PRIORITY FILING DATE: 2001-07-30
PRIORITY APPLICATION NUMBER: 60/062250
PRIORITY FILING DATE: 1997-10-17
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PRIORITY FILING DATE: 1998-05-07
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PRIORITY APPLICATION NUMBER: 60/084640
PRIORITY FILING DATE: 1998-05-07

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Db 1930 ATTTAGAAGAGAGAACTACATTCATGTTGGTGAAGAGATAAACCTGAAAAGAGAGTGG 1989
Qy 1742 CCTTATCTTCACCTTATCGATAAGTCAGTTTATTTGTTTCATTCGTGTACATTTTATATT 1801
Db 1990 CCTTATCTTCACCTTATCGATAAGTCAGTTTATTTGTTTCATTCGTGTACATTTTATATT 2049
Qy 1802 CTCCTTTTGACATTAATCTGTTGGCTTTTCTAATCTTGTGTTAAATATATCTATTTTACC 1861
Db 2050 CTCCTTTTGACATTAATCTGTTGGCTTTTCTAATCTTGTGTTAAATATATCTATTTTACC 2109
Qy 1862 AAAGGTATTAATATCTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGGTAAAT 1921
Db 2110 AAAGGTATTAATATCTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGGTAAAT 2169
Qy 1922 TTTTCTAAACAACTTGTATAGCCAGAGGAAACAAAGATGATATAAAATATTTGTTGCC 1981
Db 2170 TTTTCTAAACAACTTGTATAGCCAGAGGAAACAAAGATGATATAAAATATTTGTTGCC 2226
Qy 1982 CTGACAAAATAACATGATTTTCCATCCCGGAATGGTCTAGAGTTGGATTAACCTGCA 2041
Db 2227 TCTGACAAAATAACATGATTTT-CATTCTGATGGTCTAGAGTTAGATT-AACTGCA 2284
Qy 2042 TTTTAAAAAAGCTGAATTTGGAAGGAATTTGTAAGTTGGCCAAACCTTTTGTAAAA 2101
Db 2285 TTTTAAAAAAGCTGAATT---GGAATAGAAATTTGTAAGTT---GCAAGAGACTTTTGTAAAA 2338
Qy 2102 TAATTAA 2108
Db 2339 TAATTAA 2345

RESULT 15

US-09-999-833A-487
; Sequence 487, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Kuo, Sophia S.
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; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C65
; CURRENT FILING DATE: 2001-10-24
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250

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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 93.9%; Score 1979.4; DB 11; Length 2849;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;

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Qy 62 TGACATCTGCCCTGGCGGCAGAGACGAGGAGCTCAGCGGAATCCAACTGAGTAGTA 121
Db |||||
310 TGACATCTGCCCTGGCGGCAGAGACGAGGAGCTCAGCGGAATCCAACTGAGTAGTA 369
Qy 122 AATCCAGTTTCCAGCAACAGGAAACAGACGAGTCAAGATCCTCAGCATGAGAGAA 181
Db |||||
370 AATCCAGTTTCCAGCAACAGGAAACAGACGAGTCAAGATCCTCAGCATGAGAGAA 429
Qy 182 TTATTACTGTGTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCTACTATATCCAA 241
Db |||||
430 TTATTACTGTGTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCTACTATATCCAA 489
Qy 242 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGTAGGAAATATGATGGATCAACTTA 301
Db |||||
490 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGTAGGAAATATGATGGATCAACTTA 549
Qy 302 CGTTTGTGAAGATTTCGGCTTGAAGACCCAGAGATGACATATGCAAGTAGTATGTTTG 361
Db |||||
550 CGTTTGTGAAGATTTCGGCTTGAAGACCCAGAGATGACATATGCAAGTAGTATGTTTG 609
Qy 362 TAGAAGTTGAGGAACCCAGTGTGATGAACTATATTAGGGCGCTGGTGTCTGTGACTG 421
Db |||||
610 TAGAAGTTGAGGAACCCAGTGTGATGAACTATATTAGGGCGCTGGTGTCTGTGACTG 669
Qy 422 TACCAGGAAACAGATTTCCTAAGGAAATCAAAATTAGGATAGATTGTATCTGATGAAT 481
Db |||||
670 TACCAGGAAACAGATTTCCTAAGGAAATCAAAATTAGGATAGATTGTATCTGATGAAT 729
Qy 482 ATTTTCTCTGAAACAGGGTTCTGCATCCACTACAACATTGTCTGCCCACTTACACAG 541
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730 ATTTTCTCTGAAACAGGGTTCTGCATCCACTACAACATTGTCTGCCCACTTACACAG 789
Qy 542 AAGCTGTGAGTCTTTCAGTGTACCCCTTCAGCTTTCAGCTGAGGACCTGCTTAATG 601
Db |||||
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Qy 602 CTATAACTGCCCTTTAGTACCTTGGAGACCTTATTCGATATCTTGNACCAGAGATGCG 661
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850 CTATAACTGCCCTTTAGTACCTTGGAGACCTTATTCGATATCTTGNACCAGAGATGCG 909
Qy 662 AGTTGACCTTAGAAGATCTATATAGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGT 721
Db |||||
910 AGTTGACCTTAGAAGATCTATATAGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGT 969
Qy 722 TTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGAGGTAAAGATTATACA 781
Db |||||
970 TTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGAGGTAAAGATTATACA 1029

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Db	1090	TTTTC	TGGCCAGGTGTCCTCGTTTAAACGCTGTGGTGGGAACGTGCGCTGTGTCTCC	1149
Qy	902	ACAATT	CGAATGTCATGTGTCGCCAAGCAAAAGTTACTTAAAAATACCAAGAGTCC	961
Db	1150	ACAATT	CGAATGTCATGTGTCGCCAAGCAAAAGTTACTTAAAAATACCAAGAGTCC	1209
Qy	962	TTCA	GTTGAGACCAAAGACCGGTGTACGGGATTGCACAAACTCACTCACCGAGTGGCCC	1021
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Qy	1022	TGGAG	CACCATGAGGAGTGTCACTGTGTGTCAGAGGGAGCACAGGAGGATACCGCATC	1081
Db	1270	TGGAG	CACCATGAGGAGTGTCACTGTGTGTCAGAGGGAGCACAGGAGGATACCGCATC	1329
Qy	1082	ACCA	CCAGCAGCTCTTGCCCAAGACCTGTGCAGTGCAGTGGCTGATTTCTATTAGAGAACGT	1141
Db	1330	ACCA	CCAGCAGCTCTTGCCCAAGACCTGTGCAGTGCAGTGGCTGATTTCTATTAGAGAACGT	1389
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Db	1390	ATGCG	TATATCTCAATCCCTTAATCTCACTGTTTTCCTTCAAGGACCTTTCATCTCAGGAT	1449
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Qy	1262	TTGAG	AGGAGGCCCTTAAAGGACAGAGAAAAGGTCCTTCAATCGTGGAAAGAAAATTAATG	1321
Db	1510	TTGAG	AGGAGGCCCTTAAAGGACAGAGAAAAGGTCCTTCAATCGTGGAAAGAAAATTAATG	1569
Qy	1322	TTGAT	TAAATAGATACACGACTAGTTTCAGAGTTACATGTACGTAATCCACTAGCTGG	1381
Db	1570	TTGAT	TAAATAGATACACGACTAGTTTCAGAGTTACATGTACGTAATCCACTAGCTGG	1629
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Qy	1442	TGCA	AGTGAGCACCTCGATTCCGTTGCGCTTGTCTAACTCTAAAGCTCCATGTCTGGCGCT	1501
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Db	2339	TAATTAA	2345	

Search completed: November 26, 2003, 09:32:25
Job time : 529.968 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 25, 2003, 23:39:26 ; Search time 3075.92 Seconds
(without alignments)
16656.442 Million cell updates/sec

Title: US-09-852-209A-2

Perfect score: 2108

Sequence: 1 cccgcgcgtgagtgagctct.....nctttttgaaataattaa 2108

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1894.2	89.9	2826	11	BC041783 Homo sapi
2	1892.4	89.8	2655	11	BC051876 Homo sapi
3	960.2	45.6	3244	11	AK033734 Mus muscu
4	959.4	45.5	2765	11	AK052947 Mus muscu

5	957.8	45.4	3405	11	AK042767 Mus muscu
6	891.4	42.3	2893	11	BC029099 Mus muscu
7	834	39.6	999	13	BQ068266 AGENCOURT
8	796.2	37.8	969	10	BG677432 602625259
9	768	36.4	811	10	BG185961 RST4916 A
10	759.2	36.0	1142	10	BG681390 602627750
11	733.4	34.8	802	12	B1870535 603394005
12	697.2	33.1	769	14	CB309471 AGENCOURT
13	641.6	30.4	686	12	BQ015321 UI-H-ED1-
14	631.8	30.0	2502	11	AK081347 Mus muscu
15	608.2	28.9	789	12	B1911795 603065222
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17	568.4	27.0	572	13	BQ694737 1000880 H
18	567.2	27.0	695	12	B1668022 603295848
19	567.4	26.9	902	13	BUS17879 AGENCOURT
20	566.6	26.9	571	14	W63582 2b99b09.r1
21	560.6	26.6	567	12	BM827309 K-EST0099
22	559.4	26.5	696	10	BG430400 602502113
23	548.8	26.0	574	14	CA397892 cs97d11.y
24	540.4	25.6	835	10	BG681328 602627178
25	534	25.3	771	14	CB310542 AGENCOURT
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28	499.2	23.7	562	9	AU280428 AU280428
29	489.2	23.2	823	13	BUE14825 UI-M-EVO-
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45	432.2	20.5	877	10	BF137533 601780532

ALIGNMENTS

RESULT 1

BC041783

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

BC041783 2826 bp mRNA linear HTC 13-JAN-2003
Homo sapiens, Similar to platelet-derived growth factor, C
polypeptide, clone IMAGE:4614150, mRNA.

BC041783.1 GI:27692870

HTC.

Homo sapiens (human)

Homo sapiens

1 (bases 1 to 2826)

Strausberg, R.

Direct Submission

Submitted (23-DEC-2002)

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: CLONTECH

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@axil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 41 Row: 9 Column: 9
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 9994186
 This clone has the following problem: frame shifted.

FEATURES

Location/Qualifiers
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 /clone="IMAGE:4614150"
 /tissue_type="Kidney"
 /clone_lib="NIH MGC_75"
 /lab_host="DH10B"
 /note="Vector: pDNR-LIB"

BASE COUNT 870 a 519 c 591 g 846 t

ORIGIN

Query Match 89.9%; Score 1894.2; DB 11; Length 2826;
 Best Local Similarity 94.8%; Pred. No. 5.6e-298;
 Matches 2057; Conservative 1; Mismatches 38; Indels 73; Gaps 7;

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 DB |||||
 QY 189 CCGCGGTGAGTCTCTCACCCAGTCAGCGCAATGAGCTCTTCGGGCTTCCTGGC 248
 DB |||||
 QY 62 TGACATCTGCTCCGCGCCAGAGACGAGGAGTCTCAGCGGAATCCCACTGAGTAGTA 121
 DB |||||
 QY 249 TGACATCTGCTCCGCGCCAGAGACGAGGAGTCTCAGCGGAATCCCACTGAGTAGTA 308
 DB |||||
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 DB |||||
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 QY 154 -----GGAGTACAAGATCCCTCAGCATGAGAGA 180
 DB |||||
 QY 369 TGGCATAGAAAGAGAGAAAGAACATTTAAAGAGATCAAGATCCTCAGCATGAGAGA 428
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 QY |||||
 DB 1141 TATGCGTTATCTCCATCTTAATCTCAGTGTGCTTCAAGGAGCTTTCATCTTCAGGA 1200
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AK052947 2765 bp mRNA linear HTC 05-DEC-2002
Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone: D93001M08 product: platelet-derived growth factor, C polypeptide, full insert sequence.
AK052947
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, K., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
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Genome Res. 10 (11), 1757-1771 (2000)
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,

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Muranatsu, M. and Hayashizaki, Y.	QY	562	AGTTGGACTTTAGAGATCTATATAGGCCAACTTTGGCAACTTCTTTGGCAAGCTTTTGT	721
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Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,	QY	842	TTTTTCTGGCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCTGTGTCTCC	901
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Please visit our web site for further details.	QY	1082	ACACAGAGAGCTTTCGCCAGAGCTGTGCAGTGTGAGTGGCTGATTTCTATTAGAGACGT	1141
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 VERSION BC029099.1 GI:20809397
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Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 2893)
 Direct Submission
 Submitted (01-MAY-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: http://mgc.nci.nih.gov
 Contact: MGC help desk
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: http://www.hgsc.bcm.tmc.edu/cdna/
 Contact: amg@bcm.tmc.edu
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Qy 1683 TTTAGAGAAAGAGAACTACATTCATGTTTGGAGAGATAAACTGAAAAAGAGAGTGGC 1742
Db 1952 TTTTGGAGAA--AGTGGCGTCACTGTTTGGAGAAAGCACACCTGCACAGAGAGTGGC 2008
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Qy 1863 AAGTATTTAATAATCTTTTATGACAACCTAGATCAACTTATTTTATGCTTGTGTA--A 1920
Db 2128 AAGTATTTAATAATCTTTTATGACAACCTAGCAATTTATTTTATGCTTGTGTAATTT 2187
Qy 1921 TTTTCTTAAACACAATTTGTTATAGCCAGAGAAACAAGATG--GATATAAAATATGTT 1977
Db 2188 TTTTCTTAAACAGAAATTTTATAGCCAGAGAAACAAGATGATTTGATATAAAATCTTTGT 2247
Qy 1978 TGCCTGAGCAAAATACATGATNTCCATCCCGAATGGTGTAGAGTTGGATTAACCC 2037
Db 2248 TGCTCT--GACAAAAACATATGATTTT--CTTCTTGTATGGTGTAGAGCTTAGCGTCATC 2305
Qy 2038 TGCATTTTAAAAAA 2051
Db 2306 TGCATTTGAAAAAA 2319
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RESULT 7
BQ068266

LOCUS DEFINITION BQ068266 999 bp mRNA linear EST 02-APR-2002
AGENCOURT_6794408 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5770510
5', mRNA sequence.

ACCESSION BQ068266
VERSION BQ068266.1 GI:19897312
KEYWORDS EST.

SOURCE
ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 999)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)

AUTHORS

Unpublished
Contact: Robert Strausberg, Ph.D.

TITLE

Email: cgapbs-remail.nih.gov

JOURNAL

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMI2833 row: k column: 23

High quality sequence stop: 676.

FEATURES

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/clone="IMAGE:5770510"
/lab_host="DH10B"
/clone_lib="NIH MGC 121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (Scorv site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."
290 a 213 c 235 g 261 t

BASE COUNT
ORIGIN

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Best Local Similarity 98.4%; Pred. No. 1e-125;
Matches 874; Conservative 0; Mismatches 10; Indels 4; Gaps 3;
69 TGCCCTGGCGGCGGAGAGCGAGGACTCAGGGGAGATCCAGGCGAATCCAACTGAGTAGTAATTTCCA 128
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129 GTTTTCCAGCAACAGCAAGCAGGAGTACAGAGTCCCTCAGCATGAGAGATTTATAC 188
Db 61 GTTTTCCAGCAACAGCAAGCAGGAGTACAGAGTCCCTCAGCATGAGAGATTTATAC 120
189 TGTGCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCCTCATCTTATCCAGAAATAC 248
Db 121 TGTGCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCCTCATCTTATCCAGAAATAC 180
249 GGTCTTGATGAGATTTAGTAGCAGTAGAGGAAATATGATGATACAACTTACGTTTGA 308
Db 181 GGTCTTGATGAGATTTAGTAGCAGTAGAGGAAATATGATGATACAACTTACGTTTGA 240
309 TGAAGATTTGGGCTTGAAGCCAGAGATGACATATGCAAGTATGATTTGTAGAGT 368
Db 241 TGAAGATTTGGGCTTGAAGCCAGAGATGACATATGCAAGTATGATTTGTAGAGT 300
369 TGAGGACCCAGTGATGGAACCTATATTAGGGCGCTGGTGGTCTGCTACTGTACCAGG 428
Db 301 TGAGGACCCAGTGATGGAACCTATATTAGGGCGCTGGTGGTCTGCTACTGTACCAGG 360
429 AAAACAGATTTCTAAAGGAATCAAAATAGGATAGATTTGATCTGATGATTTTCC 488
Db 361 AAAACAGATTTCTAAAGGAATCAAAATAGGATAGATTTGATCTGATGATTTTCC 420
489 TTCTGAACCCAGGTTCTGCATCCCTACACATTCATGTCACAAATTCACAGAGCTGT 548
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729 AAAATCCAGAGTGGTGGATCTGAACCTTTAAACAGAGAGGTAAGATTATACAGCTGCAC 788
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789 ACTCGTAACTTCTCAGTGTCC--ATAAGGAGAACTAAAGAGAACCGATACCA-TTTT 845
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846 CTGGCCAGGTTGTCTCTCTGTTAAACGCTGTGTGGGAACTGTGCTTTGTCTCCACAA 905
Db 781 CTGGCCAGGTTGTCTCTCTGTTAAACGCTGTGTGGGAACTGTGCTTTGTCTCCACAA 840
906 TTGCAATGAATGTCAAT-GTGTCCCAAGCAAGTTACTTAAAAATACC 952
Db 841 TTGCAATGAATGTCCATGTGTCCCAAGCAAGTTACTTAAAAATACC 888
RESULT 8
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LOCUS 602625259F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4750095 5',
DEFINITION mRNA sequence.
ACCESSION BG677432 GI:13908829
VERSION BG677432
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1. (bases 1 to 969)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgraphs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI0604 row: f column: 16
High quality sequence stop: 764.
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/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: oligo drt. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 257 a 223 c 221 g 268 t
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Query Match 37.8%; Score 796.2; DB 10; Length 969;
Best Local Similarity 90.9%; Pred. No. 1.4e-119;
Matches 881; Conservative 0; Mismatches 83; Indels 5; Gaps 3;
736 AGAGTGGTGGATCTGAACCTTTCTAACAGAGAGGTAAGATTATACAGCTGCACACCTCGT 795
Db 1 ATAGTGGTGGATCTGAACCTTTCTAACAGAGAGGTAAGATTATACAGCTGCACACCTCGT 60
796 AACTTCTCAGTGTCCATTAAGGAGAACTAAAGAGAACCGATACCA-TTTTCTGGCCAGGT 855
Db 61 AACTTCTCAGTGTCCATTAAGGAGAACTAAAGAGAACCGATACCA-TTTTCTGGCCAGGT 120

856 TGTCTCTGTTAAACGCTGTGGTGGAACTGTGCTGTTGTCTCCCAAAATGCAATGAA 915
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121 TGTCTCTGTTAAACGCTGTGGTGGAACTGTGCTGTTGTCTCCCAAAATGCAATGAA 180
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916 TGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACCAAGAGTCTTTCAGTTGAGACCA 975
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181 TGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACCAAGAGTCTTTCAGTTGAGACCA 240
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976 AAGACCGGTGTCCAGGAGTGTCAAAATCACTACCGACGTGGCCCTGGAGCACCATGAG 1035
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241 AAGACCGGTGTCCAGGAGTGTCAAAATCACTACCGACGTGGCCCTGGAGCACCATGAG 300
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1036 GAGTGTGACTGTGTGTCAGAGGGAGCACAGAGGATAGCCGATACCAACACAGAGCTC 1095
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301 GAGTGTGACTGTGTGTCAGAGGGAGCACAGAGGATAGCCGATACCAACACAGAGCTC 360
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1096 TTGCCACAGAGTGTGCTGAGTGGCTGATCTTATTAGAGAACTATGCGTTATCTCCA 1155
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361 TTGCCACAGAGTGTGCTGAGTGGCTGATCTTATTAGAGAACTATGCGTTATCTCCA 420
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1156 TCCTTAATCTCAGTTGTTGCTTCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATCT 1215
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421 TCCTTAATCTCAGTTGTTGCTTCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATCT 480
Qy
1216 GAAAGAGGAGACATCAAAAGAAATAGAGTTGTGCAACAGCTCTTTTGAGAGAGGCT 1275
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481 GAAAGAGGAGACATCAAAAGAAATAGAGTTGTGCAACAGCTCTTTTGAGAGAGGCT 540
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1276 AAAGAGCAGGAGAAAGTCTCAATCGTGAAGAAATTA--AATGTTGTTAAT 1332
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1393 CAGTCTTTCAGTACGGCTTGGGTATGTGAGTACAGAGAAATTAAGTGTGCAAGTGAGC 1452
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1453 ACCTGATTCGCTGCTTCTTAATCT--TAAAGTCCATGCTCGGGCTAAATCGTAT 1511
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1512 AAAATCTGATTTTCTTTTCTTTTCTTCTATATTCATATGTAAACACAGAACTTCT 1571
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781 AAGATCTGATTTCTACTACGGTCTGGGGCCACTATTCCTTTTAAACACAGAACTTCT 840
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1572 ATGTACTACAAACCTGTTTAAAGAACTATGTGCTATGAAATTAACCTGTGTCT 1631
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841 TTGTTCTACAACTGTTTCCACACGGGCACTATGTGCGCTTTGAAATTAACCTGTGTC 900
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1632 TGCTGATAGGACAGACTGATTTTCA--TATTCTTATTAAATTTCTGCCATTTAGAG 1690
Db
901 GGGCCATAGGACCCAGGATTTCTCATATTCCTTTGTAAATTTCTGCCATTTGACAG 960
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Db
961 CACATCTCT 969

RESULT 9
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DEFINITION BG185961
ACCESSION BG185961
VERSION BG185961.1 GI:13707648
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 811)

AUTHORS

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,
Lerner, J., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith,
E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher,
J., Danzig, J., and Ducar, M.

TITLE

Creation of genome-wide protein expression libraries using random
activation of gene expression

JOURNAL

Nat. Biotechnol. 19 (5), 440-445 (2001)

MEDLINE

21227151

PUBMED

11329013

COMMENT

Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scaine@atersys.com

FEATURES

High quality sequence stop: 485.
Location/Qualifiers
1..811

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
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/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

BASE COUNT

225 a 172 c 195 g 216 t

ORIGIN

Query Match 36.4%; Score 768; DB 10; Length 811;
Best Local Similarity 97.8%; Pred. No. 5.4e-115;
Matches 788; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

Qy 351 GTATGATTTGTAGAAGTTG--AGGAAACCCAGTGTGGAACCTATATTAGGCGCTGGTGTG 409
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Qy 410 GTTCTGTGTACGTACAGGAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTG 469
Db 65 GTTCTGTGTACGTACAGGAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTG 124
Qy 470 TATCTGTGATATATTTCTCTGAACCCAGGTTCTGCATCCATCAACATTTGTCATGC 529
Db 125 TATCTGTGATATATTTCTCTGAACCCAGGTTCTGCATCCATCAACATTTGTCATGC 184
Qy 530 CACAATTCACAGAAGCTGTGATCCTTCAGTGTACCCCTTCAGCTTTCAGCTGGAC 589
Db 185 CACAATTCACAGAAGCTGTGATCCTTCAGTGTACCCCTTCAGCTTTCAGCTGGAC 244
Qy 590 TGCTTAATAAGCTATACTGCTTCTAGTCTGGAAGACCTTATTCGATATCTTGAAC 649
Db 245 TGCTTAATAAGCTATACTGCTTCTAGTCTGGAAGACCTTATTCGATATCTTGAAC 304
Qy 650 CAGAGATGCGAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCA 709
Db 305 CAGAGATGCGAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCA 364
Qy 710 AGGCTTTTGTTTTGGAAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAAACAGAGGAG 769
Db 365 AGGCTTTTGTTTTGGAAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAAACAGAGGAG 424
Qy 770 TAAGATTATACAGTGCACACCTGTAATCTTCAGTGTCCATAGGAGAACTAAAGA 829
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Qy 830 GAAACGATACCAATTTTCTGGCCAGGTTCTCTCTGTTAAACGCTGTGGTGGCAACTGTG 889
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Db |||||
QY 950 ACCACGAGGTCCTTTGAGTGGAGACCAAGACCGGTGTGACGGGATTCACAAATCACTCA 1009
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QY 1010 CCGACGTGGCCCTGGAGCACCATGAGGAGTGCTGCTGTGCTGAGGGGAGCACAGAG 1069
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QY 665 CCGACGTGGCCCTGGAGCACCATGAGGAGTGCTGCTGTGCTGAGGGGAGCACAGAG 724
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QY 1070 GATAGCCGCATCACCACGAGCTCTTTGCCAGAGCTGTGCTGCTGAGTGGCTGATTC 1129
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QY 725 GATAGCCGCATCACCACGAGCTCTTTGCCAGAGCTGTGCTGCTGAGTGGCTGATTC 784
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QY 1130 ATTAGAGAACGTATGCGTTATCTCCA 1155
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QY 785 ATTAGAGAACGTATGCGTTATCTCCA 810
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RESULT 10
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LOCUS mRNA sequence.
DEFINITION
ACCESSION BG681390
VERSION BG681390.1 GI:13912787
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1142)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL0610 row: d column: 13
High quality sequence stop: 803.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="DH10B (T1 phage-resistant)"
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/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5kb Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 364 a 241 c 288 g 249 t
ORIGIN

Query Match 36.0%; Score 759.2; DB 10; Length 1142;
Best Local Similarity 96.3%; Pred. No. 1.3e-113;
Matches 809; Conservative 0; Mismatches 28; Indels 3; Gaps 3;

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Db |||||
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Db |||||
QY 163 GAGGATGGCAGTTGGACTTTAGAGATCTATATAGGCCAACTTCGCAACTTCTTTGGCAAG 222
Db |||||
QY 712 GCTTTTGTGTTTGAAGAAAATCCAGAGTGGTGAATCTGAACTTTCTTAACAGAGAGGTA 771
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QY 223 GCTTTTGTGTTTGAAGAAAATCCAGAGTGGTGAATCTGAACTTTCTTAACAGAGAGGTA 282
Db |||||
QY 772 AGATTATACAGTCCACCTCGTAACCTTCTCAGTGTCCATAAGGGAGAGTAAGAGA 831
Db |||||
QY 283 AGATTATACAGTCCACCTCGTAACCTTCTCAGTGTCCATAAGGGAGAGTAAGAGA 342
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QY 832 ACCGATACCAATTTCTGSCCAGGTTGCTCTCTGTTAAACCGCTGTGGTGGCAACTGTGCC 891
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QY 343 ACCGATACCAATTTCTGSCCAGGTTGCTCTCTGTTAAACCGCTGTGGTGGCAACTGTGCC 402
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QY 583 TAGCGCATCACCAAGCAGCTCTTGTCCAGAGCTGTGCAAGTGTGAGTGGCTGATTCAT 642
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QY 702 TCTTCAGGATTTACAGTGCATCTTGAAAGAGGAGACATCAACAGAAATTAGGAGTTGTGC 761
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QY 1252 AACAGCTCTTTTGAGAGAGGCTTAAAGGACAGGAGAAAGGTCTTC-AACTGGGAAAG 1310
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QY 822 AAAATTAATGTTGTTAATTAATAGATCACAGGATGTTTCAAGGTTACCATGTACGTAAAT 881
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RESULT 11
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LOCUS mRNA sequence.
DEFINITION
ACCESSION BI870535
VERSION BI870535.1 GI:16044208
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 802)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM12030 row: i column: 02
High quality sequence stop: 791.
Location/Qualifiers
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/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: Not I; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH MGC Library."
208 t

BASE COUNT 227 a 169 c 198 g 208 t

ORIGIN

Query Match 34.8%; Score 733.4; DB 12; Length 802;
Best Local Similarity 97.8%; Pred. No. 2.3e-109;
Matches 787; Conservative 0; Mismatches 11; Indels 7; Gaps 4;

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QY 725 GAAGAAAATCCAGAGTGGTGATCTGAACCTTTTAAACAGAGGAGGTAAGATTATACAGCT 784
DB 58 GAAGAAAATCCAGAGTGGTGATCTGAACCTTTTAAACAGAGGAGGTAAGATTATACAGCT 117

QY 785 GCACACTCGTACTTCTCAGTCTCCATAGGGAAGCACTAAAGAGAACCGATACCATTT 844
DB 118 GCACACTCGTACTTCTCAGTCTCCATAGGGAAGCACTAAAGAGAACCGATACCATTT 177

QY 845 TCTGGCCAGGTTCTCTCTGTTTAAACGCTGTGGTGGAACTGTGCTGTGTTGTCACCA 904
DB 178 TCTGGCCAGGTTCTCTCTGTTTAAACGCTGTGGTGGAACTGTGCTGTGTTGTCACCA 237

QY 905 ATTGCAATGAATGCAATGTGTCACGAAAGTTACTTAAATAATACCAAGGTCCTTC 964
DB 238 ATTGCAATGAATGCAATGTGTCACGAAAGTTACTTAAATAATACCAAGGTCCTTC 297

QY 965 AGTTGACCAAGACCGGTGTGAGGGGATTCACAAATCACTACCGAGTGGCCCTGG 1024
DB 298 AGTTGACCAAGACCGGTGTGAGGGGATTCACAAATCACTACCGAGTGGCCCTGG 357

QY 1025 AGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGAGGATAGCCGATCACC 1084
DB 358 AGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGAGGATAGCCGATCACC 417

QY 1085 ACCAGAGCTCTTGGCCAGAGCTGTGCAAGTGTGCTGATTCATTATAGAAAGCATG 1144
DB 418 ACCAGAGCTCTTGGCCAGAGCTGTGCAAGTGTGCTGATTCATTATAGAAAGCATG 477

QY 1145 CGTTATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCA 1204
DB 478 CGTTATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCA 537

QY 1205 CAGTGCATCTGAAAGAGGAGACATCAAAAGAAATAGGAGTGTGCAACAGCTCTTTTG 1264
DB 538 CAGTGCATCTGAAAGAGGAGACATCAAAAGAAATAGGAGTGTGCAACAGCTCTTTTG 597

QY 1265 AGAGGAGGCTTAAAGGACGAGGAGAAAGGCTTCAATCGTGGAAAGAAAT-AAAATGTT 1323
DB 598 AGAGGAGGCTTAAAGGACGAGGAGAAAGGCTTCAATCGTGGAAAGAAAT-AAAATGTC 657

QY 1324 GTATTAAATAGATCACCAGTAGTTTTCAGAGTTACCATGTACGATTTCACCTAGTGGGT 1383
DB

DB 658 GTATTAAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGATTTCCTAGCTGGGT 717

QY 1384 TCTGTATTTTCAGTCTTTTCGATACGCTTAGCGTAAATGTTCAGTACAGGAAAAAAGTGTG 1443
DB TCTGTATTTTCAGTCTTTTCGATACGCTTAGCGTAAATGTTCAGTACAGGAAAAAAGTGTG 776

QY 1444 CAAAGTACGACCTGATTCGCTTGGC 1468
DB 777 CAAAGTACGACCTGATTCGCTTGGC 801

RESULT 12
CB309471
LOCUS
DEFINITION
AGENCOURT 11834776 NICHDRh.Ov1 Macaca mulatta cdna clone
IMAGE:6893055 5', mRNA sequence.
CB309471
CB309471.1 GI:28832181
EST.
Macaca mulatta (rhesus monkey)
ORGANISM
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
1 (bases 1 to 769)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaps-z@mail.nih.gov
Tissue Procurement: Dr. Elliot Spindel
CDNA Library Preparation: CLONTECH
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM3156 row: 1 column: 14
High quality sequence stop: 590.
Location/Qualifiers
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/organism="Macaca mulatta"
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/db_xref="taxon:9544"
/clone="IMAGE:6893055"
/tissue_type="Ovary"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHDRh.Ov1"
/notes="Organ: ovary; Vector: pDNR-LIB; Site 1: Sfi I; Site 2: Sfi I; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.0-4.0 kb. Tissue pooled from pre-pubertal, post pubertal and menopausal monkeys. Constructed by Clontech. Note: this is a NICHDRh.Ov1 library."
220 a 158 c 188 g 202 t 1 others

BASE COUNT 220 a 158 c 188 g 202 t 1 others

ORIGIN

Query Match 33.1%; Score 697.2; DB 14; Length 769;
Best Local Similarity 96.0%; Pred. No. 1.7e-103;
Matches 725; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 609 TGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACAGAGATAGGAGTGGGA 668
DB 3 TGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACAGATAGGAGTGGGA 62

QY 669 CTTAGAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGCTTTTGTGGAAG 728
DB 63 CTTAGAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGCTTTTGTGGAAG 122

QY 729 AAAATCCAGAGTGGTGGATCTGAACCTTCTAAACAGAGGAGTAAAGATTATACAGCTGCAC 788
DB 123 AAAATCCAGAGTGGTGGATCTGAACCTTCTAAACAGAGGAGTAAAGATTATACAGCTGCAC 182

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QY 789 ACTCGTAACTTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACCGATACCAATTTCTG 848
Db 183 ACTCGTAACTTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACCGATACCAATTTCTG 242
QY 849 GCCAGTTTCTCTCTGGTTAAACCGTGTGGTGGAACTGTGCTGTGCTGTCTCCACAATTG 908
Db 243 GCCAGTTTCTCTCTGGTTAAACCGTGTGGGAGGAACGTGCTGTGCTGTCTCCACAATTG 302
QY 909 CAATGAATGTCAATGTGTCACAGCAAAAGTTACTTAAATAATACCAAGAGTCTCTCAGTT 968
Db 303 CAATGAATGTCAATGTGTCACAGCAAAAGTTACTTAAATAATACCAAGAGTCTCTCAGTT 362
QY 969 GAGACCAAAAGCCGGTGTGAGGGGATTGCACAAATCACTCACGAGTGGCCCTGGAGCA 1028
Db 363 GAGACCAAAAGCTGGTGTGAGAGGATTGCATAATCACTCACTGATGTGGCCCTAGAGCA 422
QY 1029 CCATGAGGAGTGTGATGTGTGTCAGAGGAGACACAGGAGATAGCCGATCACCACTA 1088
Db 423 CCATGAGGAGTGTGATGTGTGTCAGAGGAGACACAGGAGATAGCCGATCACCACTA 482
QY 1089 GCAGCTCTTGCACAGAGCTGTGCAGTGCAGTGGCTGATTCATTAGAGAACGTATCGTT 1148
Db 483 GCAGCTCTTGCACAGAGCTGTGCAGTGCAGTGGCTGATTCATTAGAGAACGTATCGTT 542
QY 1149 ATCTCCATCTTAACTCAGTGTGTTTCTTCAAGGACCTTTCATCTTCAGGATTTACAGT 1208
Db 543 ATCTCCATCTTAACTCAGTGTGTTTCTTCAAGGACCTTTCATCTTCAGGATTTACAGT 602
QY 1209 GCATTCGAAAGAGGAGACATCAACAGAAATAGGAGTTGTGCAACAGCTCTTTTGAGAG 1268
Db 603 GCATTCGAAAGAGGAGACATCAACAGAAATAGGAGTTGTGCAACAGCTCTTTTGAGAG 662
QY 1269 GAGGCTCTTAAAGGACAGGAGAAAGGCTTCAATCGTGGAAAGAAATTAATGTTGATT 1328
Db 663 GAGGCTCTTAAAGGACAGGAGAAAGGCTTCAATCGTGGAAAGAAATTAATGTTGATT 722
QY 1329 AATAGATACACAGCTAGTTT-CAGAGTTACCATG 1362
Db 723 AATAGCTCACAGCTAGTTTGCAGAGTTACCATG 757

RESULT 13
BQ015321/c
LOCUS
DEFINITION
  UT-H-ED1-axw-j-04-0-UI.s1 NCI CGAP_ED1 Homo sapiens cDNA clone
  IMAGE:5834595 3', mRNA sequence.
ACCESSION
  BQ015321
VERSION
  BQ015321.1 GI:19740222
KEYWORDS
  EST.
SOURCE
  Homo sapiens
  Organism
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 686)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
JOURNAL
  Unpublished
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgaps-r@mail.nih.gov
  Tissue Procurement: Dr. Jose Mercuende
  cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Clone distribution information can be found
  through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
  Seq primer: M13 FORWARD
  POLYA=Yes.
  Location/Qualifiers
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    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"

FEATURES
  source
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/clone="IMAGE:5834595"
/issue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_ED1"
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site: 1; EcoR I;
Site 2: Not I; NCI CGAP ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line C55. The library was constructed according to Bonaïdo
Lennon and Soares, Genome Research, 6:791-806, 1996.
First strand cDNA synthesis was primed with an oligo-dT
primer containing a Not I site. Double stranded cDNA was
ligated to an EcoR I adaptor, digested with Not I, and
cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG LIB=UI-H-ED1
TAG_TISSUE=chondrosarcoma
TAG_SEQ=CGTCAAGGCT"
```

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BASE COUNT 197 a 152 c 130 g 207 t
ORIGIN
Query Match 30.4%; Score 641.6; DB 12; Length 686;
Best Local Similarity 98.8%; Pred. No. 1.9e-94;
Matches 666; Conservative 1; Mismatches 5; Indels 2; Gaps 2;
QY 974 CAAAGACCGGTGTGAGGGGATTCACAAATCACTCACCGAGTGGCCCTGAGGACCATG 1033
Db 686 CAAAGACCGGTGTGCA-GGGATTGCAAAATCACTCACCGAGTGGCCCTGAGGACCATG 628
QY 1034 AGCAGTGTGACTGTGTGTCAGAGGAGACAGAGGATAGCGCATCACACGAGCAGC 1093
Db 627 AGCAGTGTGACTGTGTGTCAGAGGAGACAGAGGATAGCGCATCACACGAGCAGC 568
QY 1094 TCTTGCCAGAGCTGTGCAGTGGCTGATTCTATTAGAGAACGATATGCGTTATCTC 1153
Db 567 TCTTGCCAGAGCTGTGCAGTGGCTGATTCTATTAGAGAACGATATGCGTTATCTC 508
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QY 1154 CATCTTAACTCAGTGTGTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCAAT 1213
Db 507 CATCTTAACTCAGTGTGTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCAAT 448
QY 1214 CTGAAGAGAGAGACATCAAAACAGAAATTAGGAGTTGTGCAACAGCTCTTTTGAAGAGGAGC 1273
Db 447 TTGAAGAGAGAGACATCAAAACAGAAATTAGGAGTTGTGCAACAGCTCTTTTGAAGAGGAGC 388
QY 1274 CTAAAGGACAGGAGAAAGGCTTTCATCTGTGAAAGAAATAATAATTAATAATA 1333
Db 387 CTAAAGGACAGGAGAAAGGCTTTCATCTGTGAAAGAAATAATAATTAATAATA 328
QY 1334 GATCACCGAGTGTTCAGAGTTTACCATGTACCTGATTCCTAGCTAGCTGGTCTCTGTTATTC 1393
Db 327 GATCACCGAGTGTTCAGAGTTTACCATGTACCTGATTCCTAGCTAGCTGGTCTCTGTTATTC 268
QY 1394 AGTTCTTTTCATACCGCTTAGGGTAAATGTGAGTACAGGAGAAACCTGTGCAAGTGAGCA 1453
Db 267 AGTTCTTTTCATACCGCTTAGGGTAAATGTGAGTACAGGAGAAACCTGTGCAAGTGAGCA 208
QY 1454 CCTGATTCCGCTTGCCTTAACTCTAAAGCTCCATGTCTCTGGGCTTAAATCGTATAA 1513
Db 207 CCTGATTCCGCTTGCCTTAACTCTTAAAGCTCCATGTCTCTGGGCTTAAATCGTATAA 148
QY 1514 AATCTGGA-TTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTGTAACCGAGACATTTCTA 1572
Db 147 AATCTGGA-TTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTGTAACCGAGACATTTCTA 88
QY 1573 TGTACTACAAACCTGGTTTTTAAAGAGAACTATGTTGCTATGAATTAATTAATTTGTCRT 1632
Db 87 TGTACTACAAACCTGGTTTTTAAAGAGAACTATGTTGCTATGAATTAATTAATTTGTCRT 28
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Qy	640	TATCTTGAACCCAGAGAGATGCGAGTTGGACTTGAAGATCTATATAGGCCAACTTGGCAA	699
Db	690	TATCTTGAACCCAGAGAGATGCGAGTTGGACTTGAAGATCTATATAGGCCAACTTGGCAA	749
Qy	700	CTTCTTGGCAAGGCTTTTGTGTTTGGAAAGAAA	732
Db	750	CTTCTTGGCAAGGCTTCGGTTTGGAAAGAAA	782

Search completed: November 26, 2003, 05:47:45
Job time : 3097.58 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:55:13 ; Search time 35.9375 Seconds
(without alignments)
1523.775 Million cell updates/sec

Title: US-09-852-209a-3
Perfect score: 1858
Sequence: 1 MSIFGLLVTSALAGQRGT.....DVALEHHECDVCVRGSGTG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1858	100.0	345	21	AA1984557
2	1858	100.0	345	23	AA13212
3	1851	99.6	345	20	AA13679
4	1851	99.6	345	20	AA11766
5	1851	99.6	345	20	AA13023
6	1851	99.6	345	21	AA14857
7	1851	99.6	345	21	AA124250
8	1851	99.6	345	21	AA14322
9	1851	99.6	345	21	AA10633

10	1851	99.6	345	21	AA10635	Human VEGF-X prote
11	1851	99.6	345	21	AA10644	Human VEGF-X prote
12	1851	99.6	345	21	AA10650	Human 990126veg p
13	1851	99.6	345	21	AA10651	Human VEGF-X prote
14	1851	99.6	345	21	AA19578	Human PRO200 (vasc
15	1851	99.6	345	21	AA13414	Human PRO200 prote
16	1851	99.6	345	21	AA12412	Human PRO1713 prote
17	1851	99.6	345	21	AA101419	Human TANGO 128.
18	1851	99.6	345	21	AA196858	Human growth facto
19	1851	99.6	345	21	AA195285	Bone morphogenic p
20	1851	99.6	345	22	AA15603	Human zveg3 polyp
21	1851	99.6	345	22	AA108485	Polypeptide for hu
22	1851	99.6	345	22	AA112314	Human PRO200 polyp
23	1851	99.6	345	22	AA174028	Human VEGF/PDGF-li
24	1851	99.6	345	22	AA102649	Human LP8, a PDGF-
25	1851	99.6	345	22	AA100997	Human zveg3 prote
26	1851	99.6	345	22	AA150980	Human PRO200 prote
27	1851	99.6	345	22	AA149895	Human angiogenesis
28	1851	99.6	345	22	AA153074	Human vascular end
29	1851	99.6	345	23	AA179984	Human VEGF-like pr
30	1851	99.6	345	23	AA182899	Human VEGF/PDGF-li
31	1851	99.6	345	23	AA181331	Human zveg3. Hom
32	1851	99.6	345	23	AA147889	Human zveg3 prote
33	1851	99.6	345	23	AA176684	Human growth facto
34	1851	99.6	345	24	AA166712	Human PRO polypept
35	1851	99.6	345	24	AA166988	Human secreted/tra
36	1851	99.6	345	24	AA159791	Novel secreted and
37	1851	99.6	345	24	AA161152	Human PRO200 polyp
38	1851	99.6	345	24	AA161152	Human vascular end
39	1851	99.6	345	24	AA1610639	Human VEGF-X prote
40	1851	99.6	345	21	AA10634	Human VEGF-X homol
41	1843	99.2	345	21	AA10636	Human VEGF-X prote
42	1843	99.2	345	21	AA10636	Human growth facto
43	1843	99.2	345	21	AA10640	Human VEGF-X prote
44	1745	93.9	354	21	AA10640	Human VEGF-X prote
45	1745	93.9	354	21	AA10641	Human VEGF-X prote

ALIGNMENTS

RESULT 1
AA1984557
ID AA1984557 standard; Protein; 345 AA.
AC AA1984557;
DT 25-JUL-2000 (first entry)

XX Amino acid sequence of platelet-derived growth factor C (PDGF-C).
DE Platelet-derived growth factor C; PDGF-C; cell proliferation;
KW growth factor; heparin; connective tissue; wound healing; VEGF-F;
KW fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;
KW choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia;
KW lung carcinoma; erythroleukemia; tissue remodelling.

XX Homo sapiens.
XX WO2000018212-A2.
XX 06-APR-2000

XX 30-SEP-1999; 99WO-US222668.
XX 30-SEP-1998; 98US-0102461.
XX 12-NOV-1998; 98US-0108109.
XX 03-DEC-1998; 98US-0110749.
XX 18-DEC-1998; 98US-0113002.
XX 21-MAY-1999; 99US-0135426.
XX 15-JUL-1999; 99US-0144022.

XX (LUDW-) LUDWIG INST CANCER RES.

PA (UYHE-) UNIV HELSINKI LICENSING LTD.
 XX Eriksson U, Aase K, Lee X, Ponten A, Uutela M, Alitalo K;
 PI Oestman A, Heldin C, Betsholtz C;
 XX WPI; 2000-292954/25.
 DR N-PSDB; AAL12523.
 XX Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,
 PT differentiation, growth and motility of cells expressing the PDGF-C
 PT receptor -
 XX Claim 27; Fig 2; 135pp; English.
 PS
 XX The present sequence represents human platelet-derived growth factor C
 CC (PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the
 CC ability to stimulate and enhance proliferation or differentiation,
 CC and/or growth or motility of cells expressing a PDGF-C receptor.
 CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell
 CC proliferation, preferably in combination with one other growth factor
 CC and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also
 CC be used for stimulating connective tissue or wound healing. The
 CC PDGF-C polypeptide can be enzymatically processed to generate the active
 CC truncated form of PDGF-C and used to regulate the receptor-binding
 CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
 CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.
 CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour
 CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
 CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
 CC and erythroleukemia, can be identified by testing for expression of
 CC PDGF-C. PDGF-C antagonists can also be used to inhibit tissue
 CC remodelling during invasion of tumour cells into a normal population of
 CC cells. Antagonists can also be used to treat fibrotic conditions,
 CC especially found in the lung, kidney or liver.
 XX
 SQ Sequence 345 AA;

Query Match 100.0%; Score 1858; DB 21; Length 345;
 Best Local Similarity 100.0%; Pred. No. 1.4e-179;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSFLGLLVTSALAGQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
 DB 1 MSFLGLLVTSALAGQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
 QY 61 PRPHTYPRNTVLVRLVAEENWVWLTDFERFGLDPEDDICKYDFVEVEEESDGTIL 120
 DB 61 PRPHTYPRNTVLVRLVAEENWVWLTDFERFGLDPEDDICKYDFVEVEEESDGTIL 120
 QY 121 GRWCGSTVPGKQISKGNQIRIRFVSDYFPPSPGFCIHYNIVMPQTEAVSPVLPPSA 180
 DB 121 GRWCGSTVPGKQISKGNQIRIRFVSDYFPPSPGFCIHYNIVMPQTEAVSPVLPPSA 180
 QY 181 LPDLNNATATSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVGRKSRVDNL 240
 DB 181 LPDLNNATATSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVGRKSRVDNL 240
 QY 241 LTBVRLYSTCPNRFVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECCVPSK 300
 DB 241 LTBVRLYSTCPNRFVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECCVPSK 300
 QY 301 VTKKYHEVLQRLPKTGVGRGLHSLTDVALEHHEECDCVCRGSGTG 345
 DB 301 VTKKYHEVLQRLPKTGVGRGLHSLTDVALEHHEECDCVCRGSGTG 345

RESULT 2
 AAEL3212
 ID AAEL3212 standard; Protein; 345 AA.
 XX
 AC AAEL3212;
 XX
 DT 12-FEB-2002 (first entry)

XX Human platelet-derived growth factor (PDGF-C) protein.
 DE
 XX Human; transgenic animal; platelet derived growth factor C; PDGF-C;
 KW cardiac hypertrophy; fibrosis.
 XX Homo sapiens.
 OS
 XX WO200172132-A1.
 EN
 XX 04-OCT-2001.
 PD
 XX 28-MAR-2001; 2001WO-US09855.
 PF
 XX 28-MAR-2000; 2000US-192507P.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA Eriksson U, Li X, Ponten A, Aase K, Li H;
 PI WPI; 2002-010700/01.
 XX
 XX A transgenic animal over-expressing platelet derived growth factor C is
 PT useful to study and find therapy for disease associated with PDGF-C
 PT over-expression, including cardiac hypertrophy and fibrosis -
 XX Disclosure; Page 40-42; 48pp; English.
 XX The patent discloses a method for producing a transgenic, non-human
 CC animal over-expressing a platelet derived growth factor C (PDGF-C),
 CC or its functional fragment or analogue. The method involves introducing
 CC a transgenic PDGF-C DNA into a cell of a non-human animal, introducing
 CC the cell into a non-human animal and allowing the cell to develop into
 CC a transgenic, non-human animal. The transgenic animal is useful as a
 CC model to study disease states characterised by over-expression of PDGF-C
 CC and to find therapy for those diseases, particularly hypertrophy and
 CC fibrosis in various organs including the heart. The present sequence
 CC is PDGF-C protein from human.
 XX
 SQ Sequence 345 AA;

Query Match 100.0%; Score 1858; DB 23; Length 345;
 Best Local Similarity 100.0%; Pred. No. 1.4e-179;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSFLGLLVTSALAGQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
 DB 1 MSFLGLLVTSALAGQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
 QY 61 PRPHTYPRNTVLVRLVAEENWVWLTDFERFGLDPEDDICKYDFVEVEEESDGTIL 120
 DB 61 PRPHTYPRNTVLVRLVAEENWVWLTDFERFGLDPEDDICKYDFVEVEEESDGTIL 120
 QY 121 GRWCGSTVPGKQISKGNQIRIRFVSDYFPPSPGFCIHYNIVMPQTEAVSPVLPPSA 180
 DB 121 GRWCGSTVPGKQISKGNQIRIRFVSDYFPPSPGFCIHYNIVMPQTEAVSPVLPPSA 180
 QY 181 LPDLNNATATSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVGRKSRVDNL 240
 DB 181 LPDLNNATATSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVGRKSRVDNL 240
 QY 241 LTBVRLYSTCPNRFVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECCVPSK 300
 DB 241 LTBVRLYSTCPNRFVSIREELKRTDTIFWPGLLVKRCGNCACCLHNCNECCVPSK 300
 QY 301 VTKKYHEVLQRLPKTGVGRGLHSLTDVALEHHEECDCVCRGSGTG 345
 DB 301 VTKKYHEVLQRLPKTGVGRGLHSLTDVALEHHEECDCVCRGSGTG 345

RESULT 3
 AAY33679
 ID AAY33679 standard; Protein; 345 AA.

XX AAY33679;
 XX 11-JAN-2000 (first entry)
 XX Human VEGF-E protein.
 XX VEGF-E; human; vascular endothelial cell growth factor; wound repair;
 KW treatment; cardiovascular disorder; endothelial disorder; therapy;
 KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;
 KW angiogenic disorder; age-related macular degeneration; vascular disease;
 KW neovascularization; tumor; gene mapping.
 XX

OS Homo sapiens.

XX WO9947677-A2.

XX 23-SEP-1999.

XX 10-MAR-1999; 99WO-US05190.

XX 17-MAR-1998; 98US-0040220.

XX 02-NOV-1998; 98US-0184216.

XX (GETH) GENENTECH INC.

XX Ferrara N, Kuo SS;

XX WPI; 1999-580306/49.

XX N-PSDB; AA223691.

PT New growth factor polypeptide useful for treating cardiovascular or
 PT endothelial disorders, e.g. cardiac hypertrophy -

XX Claim 1; Fig 2; 122pp; English.

XX This invention describes the isolation of a novel human vascular
 CC endothelial cell growth factor-E (VEGF-E) polypeptide which has
 CC tranquilizer, vulnery and cardiant activity. VEGF-E can be administered
 CC therapeutically, especially by expressing encoding polynucleotides, to
 CC treat cardiovascular or endothelial disorders in mammals, especially
 CC humans. It is useful in wound repair and tissue generation and
 CC regeneration, and may especially be used to treat cardiac hypertrophy
 CC It can be combined with a carrier in pharmaceutical compositions, which
 CC can be administered to treat disorders as above. VEGF-E can be used to
 CC screen for antagonists and agonists, and the antagonists administered to
 CC treat angiogenic disorders in mammals (especially humans) e.g. cancer or
 CC age-related macular degeneration. It can be used to generate antibodies,
 CC useful therapeutically as antagonists, as above. The antibodies are also
 CC useful to detect VEGF-E polypeptide, especially to diagnose
 CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.
 CC vascular disease, or neovascularization associated with tumor formation),
 CC by contacting the antibody with a tissue sample and detecting formation
 CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding
 CC VEGF-E can be used to diagnose cardiovascular and endothelial disorders
 CC in mammals, by detecting abnormally high or low VEGF-E gene expression in
 CC tissue samples. They can also be used to diagnose a disease or
 CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a
 CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by
 CC detecting a mutation in the VEGF-E-encoding sequence isolated from a
 CC sample. They may also be used to produce probes useful to detect related
 CC sequences or for gene mapping. This sequence represents the human VEGF-E
 CC protein described in the method of the invention.

XX Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 20; Length 345;

Best Local Similarity 99.4%; Pred. No. 7e-179;

Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSLFGLLVTALAGQRGTGAENLSKFFQSSNKEQNGVQDPQHERIITVSTNGSIHS 60

Db 1 MSLFGLLVTALAGQRGTGAENLSKFFQSSNKEQNGVQDPQHERIITVSTNGSIHS 60

QY	61	PRFPHTYPRNTVLVWRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEPSDCTIL	120
DB	61	PRFPHTYPRNTVLVWRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEPSDCTIL	120
QY	121	GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPPSPGFCIHNYIMVQFTEAVSPSVLPSSA	180
DB	121	GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPPSPGFCIHNYIMVQFTEAVSPSVLPSSA	180
QY	181	LPDLNNAITAFSTLLEDIRYLEPERWOLDLEDLYRPTWLLGKAFVFGKSRVVDLNL	240
DB	181	LPDLNNAITAFSTLLEDIRYLEPERWOLDLEDLYRPTWLLGKAFVFGKSRVVDLNL	240
QY	241	LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPCLLVKRCGNACCLHNCNCCQCVPSK	300
DB	241	LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPCLLVKRCGNACCLHNCNCCQCVPSK	300
QY	301	VTKKHEVLQLRPKTGVRLGHLKSLTDVALEHHEECDCVCRGSTGG	345
DB	301	VTKKHEVLQLRPKTGVRLGHLKSLTDVALEHHEECDCVCRGSTGG	345

RESULT 4
 AAY41766
 ID AAY41766 standard; Protein; 345 AA.
 XX AC
 XX AAY41766;
 XX 07-DEC-1999 (first entry)
 XX Human PRO200 protein sequence.
 DE Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein.
 XX Homo sapiens.
 OS WO9946281-A2.
 PN 16-SEP-1999.
 XX 08-MAR-1999; 99WO-US05028.
 XX 10-MAR-1998; 98US-0077450.
 PR 11-MAR-1998; 98US-0077632.
 PR 11-MAR-1998; 98US-0077641.
 PR 11-MAR-1998; 98US-0077649.
 PR 12-MAR-1998; 98US-0077791.
 PR 13-MAR-1998; 98US-0078004.
 PR 17-MAR-1998; 98US-0040220.
 PR 20-MAR-1998; 98US-0078886.
 PR 20-MAR-1998; 98US-0078910.
 PR 20-MAR-1998; 98US-0078936.
 PR 25-MAR-1998; 98US-0078939.
 PR 26-MAR-1998; 98US-0079294.
 PR 27-MAR-1998; 98US-0079663.
 PR 27-MAR-1998; 98US-0079664.
 PR 27-MAR-1998; 98US-0079689.
 PR 27-MAR-1998; 98US-0079728.
 PR 30-MAR-1998; 98US-0079786.
 PR 30-MAR-1998; 98US-0079920.
 PR 31-MAR-1998; 98US-0079923.
 PR 31-MAR-1998; 98US-0080105.
 PR 31-MAR-1998; 98US-0080107.
 PR 31-MAR-1998; 98US-0080165.
 PR 01-APR-1998; 98US-0080194.
 PR 01-APR-1998; 98US-0080327.
 PR 01-APR-1998; 98US-0080328.
 PR 01-APR-1998; 98US-0080333.
 PR 01-APR-1998; 98US-0080334.
 PR 08-APR-1998; 98US-0081049.

PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
PA (GETH) GENENTECH INC.
XX
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
XX WPI; 1999-551358/46.
XX N-PSDB; AA234296.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders -
XX
XX Claim 12; Fig 207; 530pp; English.
PS
XX

CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AA233891 to
CC AA234338, and AA41685 to AA41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
SQ Sequence 345 AA;
Query Match 99.6%; Score 1851; DB 20; Length 345;
Best Local Similarity 99.4%; Pred. NO. 7e-179;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKQNGVDPQHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKQNGVDPQHERIITVSTNGSIHS 60
QY 61 PRPPTYPRNTVLVWRLVAEENVTQLTDFDERFGLDEDDICKYDFVEVEPSDGTIL 120
Db 61 PRPPTYPRNTVLVWRLVAEENVTQLTDFDERFGLDEDDICKYDFVEVEPSDGTIL 120
QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFPPSPGFCIHYNIVMPQTEAVSPVLPSSA 180
Db 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFPPSPGFCIHYNIVMPQTEAVSPVLPSSA 180
QY 181 LPDLNLNNAITAPSTLEDLIRYLEPERWQDLLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240
Db 181 LPDLNLNNAITAPSTLEDLIRYLEPERWQDLLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240
QY 241 LTEEVRLYSCTPRNFSVSIRBELKRTDTTFWPGCLLVKRCGNACACCLHNCNECQCVPSPK 300
Db 241 LTEEVRLYSCTPRNFSVSIRBELKRTDTTFWPGCLLVKRCGNACACCLHNCNECQCVPSPK 300
QY 301 VTKKYHEVLQRLPKTVGRGLHKSLTDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRLPKTVGRGLHKSLTDVALEHHEECDCVCRGSTGG 345
RESULT 5
AA230023
ID AA230023 standard; Protein; 345 AA.
XX
XX AA230023;
XX
DT 11-OCT-1999 (first entry)
XX
DE Human vascular endothelial growth factor related protein.
XX
KW Vascular endothelial growth factor related protein; VEGF-R protein;
KW tissue growth inhibition; tumour growth; cancer; tissue growth;
XX angiogenesis; coronary artery blockage.
OS Homo sapiens.
XX
XX WO9937671-A1.
XX
PD 29-JUL-1999.
XX
PF 26-JAN-1999; 99WO-US01574.
XX
XX 31-AUG-1998; 98US-0098548.
PR 27-JAN-1998; 98US-0072635.
PR 05-JUN-1998; 98US-0088089.
PR 24-JUN-1998; 98US-0090544.
XX
XX (ELIL) LILLY & CO ELI.
XX
XX Dou S, Na S, Song HY;

```

XX WPI; 1999-458680/38.
DR N-PSDB; AAX86352.
XX
XX A vascular endothelial growth factor related protein and related
PT polynucleotide, useful for identifying antagonists and binding
PT compounds
XX
XX Claim 1; Page 56-58; 62pp; English.
XX
XX The present sequence represents a vascular endothelial growth factor
CC related (VEGF-R) protein. VEGF-R can be used in assays to identify
CC compounds that bind to it or that antagonize its activity. VEGF-R
CC antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting
CC tissue growth. This is useful for inhibiting tumour growth and for
CC treating cancer. VEGF-R itself can be used to stimulate tissue
CC growth, angiogenesis and to treat coronary artery blockage. The
CC VEGF-R coding sequence can be used for the recombinant production of
CC the VEGF-R protein.
XX
XX Sequence 345 AA;
XX
Query Match          99.6%; Score 1851; DB 20; Length 345;
Best Local Similarity 99.4%; Pred. No. 7e-179;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLFGLLLVTSALAGORRGTOAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGTOAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHTYPRNTVLWRLVAEENVMWQLTDERFGLSDPEDDICKYDFVEEPPSDGTIL 120
Db 61 PRPHTYPRNTVLWRLVAEENVMWQLTDERFGLSDPEDDICKYDFVEEPPSDGTIL 120
QY 121 GRWCGSTVPGKQISKGNQIRIRFVSDEYFPSEFGCIHYNVMPQTEAVSPSVLPSSA 180
Db 121 GRWCGSTVPGKQISKGNQIRIRFVSDEYFPSEFGCIHYNVMPQTEAVSPSVLPSSA 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGKSRVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGKSRVDLNL 240
QY 241 LTEEVRLYSCTPRNFVSIRLEELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Db 241 LTEEVRLYSCTPRNFVSIRLEELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
QY 301 VTKKYHEVLQLRPKTVGRGLHKSITDVALEHHEEDCVCVCGSTGG 345
Db 301 VTKKYHEVLQLRPKTVGRGLHKSITDVALEHHEEDCVCVCGSTGG 345

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RESULT 6
AAB48657
ID AAB48657 standard; Protein; 345 AA.
XX
XX AAB48657;
XX
DT 09-MAR-2001 (first entry)
XX
XX Human zveg3, SEQ ID NO:33.
XX
XX Human; zveg3; zveg4 fusion; growth factor homologue; VEGF/PDGF family;
KW CUB domain; PDGF-like activity; mitogenic; osteogenic;
KW neovascularisation; tissue repair; proliferation; differentiation;
KW liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;
KW periodontal disease; bone fracture; wound healing; vulnery; ischaemia;
KW immunomodulation; hepatic.
XX
XX Homo sapiens.
XX
XX WO200066736-A1.
XX
XX 09-NOV-2000.
PD

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XX PF
XX 03-MAY-2000; 2000WO-US40047.
XX
XX 03-MAY-1999; 93US-0304216.
PR 10-NOV-1999; 93US-0164463.
PR 04-FEB-2000; 2000US-0180169.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
XX
XX WPI; 2000-687541/67.
XX N-PSDB; AAC81582.
XX
XX Growth factor homologs and the nucleic acids that encode them, useful
e.g. for treating liver damage, ischemia, multiple sclerosis and
PT Alzheimer's disease -
XX
XX Claim 48; Page 125-126; 143pp; English.
XX
XX The invention relates to the human growth factor homologue zveg4
CC (AAB48653), and nucleic acids encoding it (AAC81555). Zveg4 is a member
CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
CC growth factor) family. Zveg4 has a growth factor domain (AAB48654)
CC characterised by a PDGF cysteine knot structure, and a CUB domain
CC (AAB48655) which has a beta barrel structure. Zveg4 has PDGF-like
CC activity, having mitogenic activity on fibroblasts, vascular smooth
CC muscle cells and pericytes, and has also been shown to stimulate bone
CC growth. The invention also relates to fusion proteins comprising human
CC zveg4 or fragments thereof, particularly human zveg4/human zveg4
CC fusions; expression constructs and host cells comprising human zveg4
CC nucleic acids; the recombinant expression of human zveg4; an antibody
CC which binds to human zveg4 or a fragment thereof; a method of activating
CC a cell-surface PDGF receptor using a zveg4-derived polypeptide; a
CC method of modulating the proliferation, differentiation, migration or
CC metabolism of bone cells, comprising exposing bone cells to
CC zveg4-derived polypeptides; and a method of detecting a genetic
CC abnormality in the zveg4 gene of a patient. Zveg4 proteins and derived
CC fragments may be used to stimulate tissue development or repair, or
CC cellular differentiation or proliferation. They are particularly used for
CC the treatment or repair of liver damage, and may also be used to
CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
CC multiple sclerosis). Due to their osteogenic activity, they may be used
CC in the treatment of periodontal disease and fractures. They may also be
CC used to enhance expansion and mobilisation of haematopoietic stem cells
CC and endothelial precursor stem cells, which may be useful in the
CC treatment of ischaemia, in wound healing, and in the modulation of the
CC immune system. The present sequence represents human zveg3.
XX
XX Sequence 345 AA;

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Query Match          99.6%; Score 1851; DB 21; Length 345;
Best Local Similarity 99.4%; Pred. No. 7e-179;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLFGLLLVTSALAGORRGTOAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORRGTOAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHTYPRNTVLWRLVAEENVMWQLTDERFGLSDPEDDICKYDFVEEPPSDGTIL 120
Db 61 PRPHTYPRNTVLWRLVAEENVMWQLTDERFGLSDPEDDICKYDFVEEPPSDGTIL 120
QY 121 GRWCGSTVPGKQISKGNQIRIRFVSDEYFPSEFGCIHYNVMPQTEAVSPSVLPSSA 180
Db 121 GRWCGSTVPGKQISKGNQIRIRFVSDEYFPSEFGCIHYNVMPQTEAVSPSVLPSSA 180
QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGKSRVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLIRPTWQLLGKAFVFGKSRVDLNL 240
QY 241 LTEEVRLYSCTPRNFVSIRLEELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300

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CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.

XX Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 21; Length 345;
 Best Local Similarity 99.4%; Pred. No. 7e-179;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFGLLLVTSALAGQRGTQAESNLSSKFQSSNKEQGVQDPQHERIITVSTNGSIHS 60
 DB 1 MSFGLLLVTSALAGQRGTQAESNLSSKFQSSNKEQGVQDPQHERIITVSTNGSIHS 60

QY 61 PRFHTYPRNTLVWRLVAEENWVQLTDFERFGLDEPDICKYDFVEEPPSDGTIL 120
 DB 61 PRFHTYPRNTLVWRLVAEENWVQLTDFERFGLDEPDICKYDFVEEPPSDGTIL 120

QY 121 GRWCGSTVFGKQISKGNQIRIRFVSDYFPEFGFCIHYNVMPQFTEAVSPVLPPSA 180
 DB 121 GRWCGSTVFGKQISKGNQIRIRFVSDYFPEFGFCIHYNVMPQFTEAVSPVLPPSA 180

QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQLDLELYRPTWLLGKAFVFGKRSRVVDLNL 240
 DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQLDLELYRPTWLLGKAFVFGKRSRVVDLNL 240

QY 241 LTBVRLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPSK 300
 DB 241 LTBVRLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPSK 300

QY 301 VTKYHEVLQRPKTGVRGLHKSITDVALEHHEEDCVCRGSTGG 345
 DB 301 VTKYHEVLQRPKTGVRGLHKSITDVALEHHEEDCVCRGSTGG 345

RESULT 9

AAB10633
 ID AAB10633 standard; Protein; 345 AA.

XX AAB10633;

XX 19-JAN-2001 (first entry)

XX Human RACE generated VEGF-X protein.

XX VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;
 KW anti-rheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
 KW venous sore; diabetic ulcer; burns; skin graft growth.

OS Homo sapiens.

XX WO200037641-A2.

XX 29-JUN-2000.

XX 21-DEC-1999; 99WO-US30503.

XX 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 99US-0124967.

PR 08-NOV-1999; 99US-0164131.

XX (JANC) JANSEN PHARM NV.

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJJ, Gosiewska A;

PI Dhanaraj SN, Xu J;

XX

DR WPI; 2000-442669/38.

XX N-PsDB; AAA71951.

XX New vascular endothelial growth factor protein, useful for treating or
 PT preventing diseases associated with inappropriate angiogenesis activity
 PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX Disclosure; Fig 6; 127pp; English.

CC This invention describes a novel vascular endothelial growth factor-X
 CC (VEGF-X) protein (Ia) and its encoding polynucleotide (Iia) which has
 CC vulnary, cytostatic, anti-rheumatic, antiarthritic, antipsoriatic and
 CC anti-diabetic activity and acts as an angiogenesis and vascularization
 CC regulator. An antisense molecule of the invention is useful for treating
 CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
 CC retinopathy by inhibiting angiogenic activity or inappropriate
 CC vascularization including formation and proliferation of new blood
 CC vessels, growth and development of tissues, tissue regeneration and organ
 CC and tissue repair in a subject. The products of the invention are useful
 CC for preparing medicaments for treating wounds such as dermal ulcers,
 CC pressure sores, venous sores, diabetic ulcers and burns and to promote
 CC skin graft growth, tissue repair, proliferation of new blood vessels,
 CC tissue regeneration and organ repair by promoting angiogenic activity or
 CC vascularization. This sequence represents the RACE generated human VEGF-X
 CC protein described in the method of the invention.

XX Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 21; Length 345;
 Best Local Similarity 99.4%; Pred. No. 7e-179;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFGLLLVTSALAGQRGTQAESNLSSKFQSSNKEQGVQDPQHERIITVSTNGSIHS 60

DB 1 MSFGLLLVTSALAGQRGTQAESNLSSKFQSSNKEQGVQDPQHERIITVSTNGSIHS 60

QY 61 PRFHTYPRNTLVWRLVAEENWVQLTDFERFGLDEPDICKYDFVEEPPSDGTIL 120

DB 61 PRFHTYPRNTLVWRLVAEENWVQLTDFERFGLDEPDICKYDFVEEPPSDGTIL 120

QY 121 GRWCGSTVFGKQISKGNQIRIRFVSDYFPEFGFCIHYNVMPQFTEAVSPVLPPSA 180

DB 121 GRWCGSTVFGKQISKGNQIRIRFVSDYFPEFGFCIHYNVMPQFTEAVSPVLPPSA 180

QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQLDLELYRPTWLLGKAFVFGKRSRVVDLNL 240

DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQLDLELYRPTWLLGKAFVFGKRSRVVDLNL 240

QY 241 LTBVRLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPSK 300

DB 241 LTBVRLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCVPSK 300

QY 301 VTKYHEVLQRPKTGVRGLHKSITDVALEHHEEDCVCRGSTGG 345

DB 301 VTKYHEVLQRPKTGVRGLHKSITDVALEHHEEDCVCRGSTGG 345

RESULT 10

AAB10635

ID AAB10635 standard; Protein; 345 AA.

XX AAB10635;

XX 19-JAN-2001 (first entry)

XX Human VEGF-X protein #1 isolated from clones 4 and 7.

XX VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;
 KW anti-rheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
 KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
 KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
 KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;

venous sore; diabetic ulcer; burns; skin graft growth.

XX Homo sapiens.

XX WO200037641-A2.

XX 29-JUN-2000.

XX 21-DEC-1999; 99WO-US30503.

XX 22-DEC-1998; 98GB-0028377.

XX 18-MAR-1999; 99US-0124967.

XX 08-NOV-1999; 99US-0164131.

XX (JANC) JANSSEN PHARM NV.

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;

PI Dhanaraj SN, Xu J;

XX WPI; 2000-442669/38.

XX N-PSDB; AAA71955.

XX New vascular endothelial growth factor protein, useful for treating or

PT preventing diseases associated with inappropriate angiogenesis activity

PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX Disclosure; Fig 9; 127pp; English.

XX This invention describes a novel vascular endothelial growth factor-X

CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has

CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and

CC antidiabetic activity and acts as an angiogenesis and vascularization

CC regulator. An antisense molecule of the invention is useful for treating

CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic

CC retinopathy by inhibiting angiogenic activity or inappropriate

CC vascularization including formation and proliferation of new blood

CC vessels, growth and development of tissues, tissue regeneration and organ

CC and tissue repair in a subject. The products of the invention are useful

CC for preparing medicaments for treating wounds such as dermal ulcers,

CC pressure sores, venous sores, diabetic ulcers and burns and to promote

CC skin graft growth, tissue repair, proliferation of new blood vessels,

CC tissue regeneration and organ repair by promoting angiogenic activity or

CC vascularization. This sequence represents the human VEGF-X protein

CC isolated from clones 4 and 7 described in the method of the invention.

XX SQ Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 21; Length 345;

Best Local Similarity 99.4%; Pred. No. 7e-179;

Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGORRGQTQAESNLSSKFFQSSNKEQNGVQDPQHERITVTNGSIHS 60

DB 1 MSLFGLLLVTSALAGORRGQTQAESNLSSKFFQSSNKEQNGVQDPQHERITVTNGSIHS 60

QY 61 PRPHPTVNTVLVWLVAEENNVWLQTDPERFGLDEPDDICKYDFVEVEPSPDGITL 120

DB 61 PRPHPTVNTVLVWLVAEENNVWLQTDPERFGLDEPDDICKYDFVEVEPSPDGITL 120

QY 121 GRWCGSGTVPGKQISGNQIRIRFVDEYPPSPGCIHYNIVMPQFTEAVSPVLPPSA 180

DB 121 GRWCGSGTVPGKQISGNQIRIRFVDEYPPSPGCIHYNIVMPQFTEAVSPVLPPSA 180

QY 181 LPDLNLNNAITAFSTLLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDNL 240

DB 181 LPDLNLNNAITAFSTLLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDNL 240

QY 241 LTEEVLRYSCPTPNFVSIREELKRTDTIPWPGCLLVKRCGNCACCLHNCNCQCVPSK 300

DB 241 LTEEVLRYSCPTPNFVSIREELKRTDTIPWPGCLLVKRCGNCACCLHNCNCQCVPSK 300

QY 301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHECDVCRCGSTGG 345

301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHECDVCRCGSTGG 345

RESULT 11

AAAB10644

ID AAB10644 standard; Protein; 345 AA.

XX AAB10644;

XX 19-JAN-2001 (first entry)

XX Human VEGF-X protein #4.

XX VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;

KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;

KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;

KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;

KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;

XX venous sore; diabetic ulcer; burns; skin graft growth.

OS Homo sapiens.

XX WO200037641-A2.

XX 29-JUN-2000.

XX 21-DEC-1999; 99WO-US30503.

XX 22-DEC-1998; 98GB-0028377.

XX 18-MAR-1999; 99US-0124967.

XX 08-NOV-1999; 99US-0164131.

XX (JANC) JANSSEN PHARM NV.

XX Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;

PI Dhanaraj SN, Xu J;

XX WPI; 2000-442669/38.

XX N-PSDB; AAA71990.

XX New vascular endothelial growth factor protein, useful for treating or

PT preventing diseases associated with inappropriate angiogenesis activity

PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX Disclosure; Fig 30B; 127pp; English.

XX This invention describes a novel vascular endothelial growth factor-X

CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has

CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and

CC antidiabetic activity and acts as an angiogenesis and vascularization

CC regulator. An antisense molecule of the invention is useful for treating

CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic

CC retinopathy by inhibiting angiogenic activity or inappropriate

CC vascularization including formation and proliferation of new blood

CC vessels, growth and development of tissues, tissue regeneration and organ

CC and tissue repair in a subject. The products of the invention are useful

CC for preparing medicaments for treating wounds such as dermal ulcers,

CC pressure sores, venous sores, diabetic ulcers and burns and to promote

CC skin graft growth, tissue repair, proliferation of new blood vessels,

CC tissue regeneration and organ repair by promoting angiogenic activity or

CC vascularization. This sequence represents a human VEGF-X protein

CC described in the method of the invention.

XX SQ Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 21; Length 345;

Best Local Similarity 99.4%; Pred. No. 7e-179;

Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLLVTSALAGORRGQTQAESNLSSKFFQSSNKEQNGVQDPQHERITVTNGSIHS 60

DB 1 MSLFGLLLVTSALAGORRGQTQAESNLSSKFFQSSNKEQNGVQDPQHERITVTNGSIHS 60

QY 61 PRPHPTVNTVLVWLVAEENNVWLQTDPERFGLDEPDDICKYDFVEVEPSPDGITL 120

DB 61 PRPHPTVNTVLVWLVAEENNVWLQTDPERFGLDEPDDICKYDFVEVEPSPDGITL 120

QY 121 GRWCGSGTVPGKQISGNQIRIRFVDEYPPSPGCIHYNIVMPQFTEAVSPVLPPSA 180

DB 121 GRWCGSGTVPGKQISGNQIRIRFVDEYPPSPGCIHYNIVMPQFTEAVSPVLPPSA 180

QY 181 LPDLNLNNAITAFSTLLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDNL 240

DB 181 LPDLNLNNAITAFSTLLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDNL 240

QY 241 LTEEVLRYSCPTPNFVSIREELKRTDTIPWPGCLLVKRCGNCACCLHNCNCQCVPSK 300

DB 241 LTEEVLRYSCPTPNFVSIREELKRTDTIPWPGCLLVKRCGNCACCLHNCNCQCVPSK 300

QY 301 VTKKYHEVLQRPKTVGRGLHKSITDVALEHHECDVCRCGSTGG 345

Qy 61 PRFHTYPRNTVLVWRLVAVENWVQLTFDERFGLDEPDIDCKYDFVEVEPSDGTIL 120
Db 61 PRFHTYPRNTVLVWRLVAVENWVQLTFDERFGLDEPDIDCKYDFVEVEPSDGTIL 120
Qy 121 GRWCGSTVPKQKQISKGNQIRIRFVSDYFFSEPGFCIHYNVMPQFTEAVSPVLPPSA 180
Db 121 GRWCGSTVPKQKQISKGNQIRIRFVSDYFFSEPGFCIHYNVMPQFTEAVSPVLPPSA 180
Qy 181 LPDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Qy 241 LTEEVRVLYSCTPRNFSVSIREEKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
Db 241 LTEEVRVLYSCTPRNFSVSIREEKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
Qy 301 VTKYHEVLQRPKTVGRGLHKSITDVALEHHEEDCVCRCSTGG 345
Db 301 VTKYHEVLQRPKTVGRGLHKSITDVALEHHEEDCVCRCSTGG 345

RESULT 12

AA10650
ID AAB10650 standard; Protein; 345 AA.

XX AAB10650;

XX DT 19-JAN-2001 (first entry)

XX DB Human 990126vegX protein.

XX KW VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
XX venous sore; diabetic ulcer; burns; skin graft growth.

OS Homo sapiens.

XX WO200037641-A2.

XX PD 29-JUN-2000.

XX PF 21-DEC-1999; 99WO-US30503.

XX PR 22-DEC-1998; 98GB-0028377.

XX PR 18-MAR-1999; 99US-0124967.

XX PR 08-NOV-1999; 99US-0164131.

XX PA (JANC) JANSEN PHARM NV.

XX PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiewska A;

XX PI Dhanaraj SN, Xu J;

XX DR WPI; 2000-442669/38.

XX PT New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

XX PS Disclosure; Fig 11; 127pp; English.

XX CC This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (1a) and its encoding polynucleotide (11a) which has
CC vulnary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful

CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human 990126vegX protein
CC used to illustrate the method of the invention.

SQ Sequence 345 AA;

Query Match 99.6%; Score 1851; DB 21; Length 345;
Best Local Similarity 99.4%; Pred. No. 7e-179; Indels 0; Gaps 0;
Matches 343; Conservative 2; Mismatches 0;

Qy 1 MSFLGLLLVTSALAGQRRGTQAESNLSSKQFSSNKQGVQDPQHERIITVSTNGSIHS 60
Db 1 MSFLGLLLVTSALAGQRRGTQAESNLSSKQFSSNKQGVQDPQHERIITVSTNGSIHS 60

Qy 61 PRFHTYPRNTVLVWRLVAVENWVQLTFDERFGLDEPDIDCKYDFVEVEPSDGTIL 120
Db 61 PRFHTYPRNTVLVWRLVAVENWVQLTFDERFGLDEPDIDCKYDFVEVEPSDGTIL 120

Qy 121 GRWCGSTVPKQKQISKGNQIRIRFVSDYFFSEPGFCIHYNVMPQFTEAVSPVLPPSA 180
Db 121 GRWCGSTVPKQKQISKGNQIRIRFVSDYFFSEPGFCIHYNVMPQFTEAVSPVLPPSA 180

Qy 181 LPDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNL 240

Qy 241 LTEEVRVLYSCTPRNFSVSIREEKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300
Db 241 LTEEVRVLYSCTPRNFSVSIREEKRTDTIFWPGCLLVKRCGNCACCLHNCNECQCVPSK 300

Qy 301 VTKYHEVLQRPKTVGRGLHKSITDVALEHHEEDCVCRCSTGG 345
Db 301 VTKYHEVLQRPKTVGRGLHKSITDVALEHHEEDCVCRCSTGG 345

RESULT 13

AA10651
ID AAB10651 standard; Protein; 345 AA.

XX AAB10651;

XX DT 19-JAN-2001 (first entry)

XX DE Human VEGF-X protein #3.

XX KW VEGF-X; vascular endothelial growth factor; human; vulnary; cytostatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
XX venous sore; diabetic ulcer; burns; skin graft growth.

OS Homo sapiens.

XX WO200037641-A2.

XX PD 29-JUN-2000.

XX PF 21-DEC-1999; 99WO-US30503.

XX PR 22-DEC-1998; 98GB-0028377.

XX PR 18-MAR-1999; 99US-0124967.

XX PR 08-NOV-1999; 99US-0164131.

XX PA (JANC) JANSEN PHARM NV.

XX PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Gosiewska A;

XX PI Dhanaraj SN, Xu J;

XX DR WPI; 2000-442669/38.

XX New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
PS Claim 72; Fig 12; 127pp; English.
XX
XX This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnerability, cytostatic, antirheumatic, antiarthritic, angiogenic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human VEGF-X protein
CC described in the method of the invention.
XX
SQ Sequence 345 AA;
Query Match 99.6%; Score 1851; DB 21; Length 345;
Best Local Similarity 99.4%; Pred. No. 7e-179;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFLGILLVTSALAGQRGQTAESNLSSKQFSSNKGQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSFLGILLVTSALAGQRGQTAESNLSSKQFSSNKGQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHTYPRNTLVWRLVAVENWVIOITDEREGLEDPEDDICKYDFVEEESDGTIL 120
DB 61 PRPHTYPRNTLVWRLVAVENWVIOITDEREGLEDPEDDICKYDFVEEESDGTIL 120
QY 121 GRWCGSTVPFGKQISKNQIRIRFVSDEYFPSEFGFCHYHNVMPQTEAVSPSLPPSA 180
DB 121 GRWCGSTVPFGKQISKNQIRIRFVSDEYFPSEFGFCHYHNVMPQTEAVSPSLPPSA 180
QY 181 LPDLINNAITAFSTLEDLRYLPERWQDLEDLYRPTWQLGKAFVFGKSRVVDLNL 240
DB 181 LPDLINNAITAFSTLEDLRYLPERWQDLEDLYRPTWQLGKAFVFGKSRVVDLNL 240
QY 241 LTEEVRLYSTCPNRFVSIRIELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
DB 241 LTEEVRLYSTCPNRFVSIRIELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
QY 301 VTKYHEVLQLRPKTGVRLHKSITDVALEHHEECDCVCRGSTGG 345
DB 301 VTKYHEVLQLRPKTGVRLHKSITDVALEHHEECDCVCRGSTGG 345
RESULT 14
AAB19578
ID AAB19578 standard; Protein; 345 AA.
AC AAB19578;
XX
DT 22-JAN-2001 (first entry)
XX
XX Human PRO200 (vascular endothelial growth factor E).
XX PRO200; vascular epithelial growth factor E; VEGF-E; human;
KW ocular disease; retinopathy; maculopathy; therapy;
KW retinitis pigmentosa; macular degeneration; retinal detachment;
KW retinal tear; macular hole; myopia; traumatic chorioretinopathy;
KW acute retinal necrosis syndrome; contusion; edema;
KW retinal vision occlusion; vascular disease; retinal vasculitis;
KW thrombocytopenic purpura; uveitis; retinal occlusion.
XX

OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT 1..14 /label= Signal_peptide
FT 15..345 /label= Mature_Pro200
FT
FT Modified-site 25..29 /note= "Asn is N-glycosylated"
FT Modified-site 55..59 /note= "Asn is N-glycosylated"
FT Modified-site 254..258 /note= "Asn is N-glycosylated"
FT Modified-site 15..21 /note= "N-myristoylation"
FT Modified-site 117..123 /note= "N-myristoylation"
FT Modified-site 127..133 /note= "N-myristoylation"
FT Modified-site 281..287 /note= "N-myristoylation"
FT Modified-site 282..288 /note= "N-myristoylation"
FT Modified-site 319..325 /note= "Amidation"
FT
XX W0200053760-A2.
XX
XX 14-SEP-2000.
XX
XX 10-MAR-2000; 2000WO-US06319.
XX
XX 12-MAR-1999; 99US-0123957.
XX
XX (GETH) GENENTECH INC.
XX
XX Ferrara N, Goddard A, Gurney AL, Hebert C, Henzel WJ, Kabakoff RC,
PI Klein RD, Kljavin IJ, Kuo SS, La Fleur M, Wood WI;
XX WPI; 2000-587437/55.
XX N-PSDB; AAA88515.
XX
XX Novel PRO polypeptides useful for preventing or rescuing retinal cells
PT from injury caused by ocular diseases such as retinitis pigmentosa,
PT retinopathy, retinal degenerative diseases, degenerative myopia,
PT uveitis -
XX
PS Claim 2; Fig 2; 140pp; English.
XX
XX The present sequence is that of human PRO200 or vascular
CC endothelial growth factor E (VEGF-E), as predicted from a cDNA
CC clone (see AAA88515) that was isolated from a glioma cell line G61
CC library using probes (see AAA88523-26) based on an expressed sequence
CC tag (see AAA88522) that showed homology to VEGF. PRO200 has a
CC predicted mol.wt. of 39,029 and a pI of about 6.06. A method for
CC producing PRO polypeptides, including PRO200, using a host cell
CC transformed with a vector comprising a PRO nucleic acid is claimed.
CC The invention relates to the use of PRO polypeptides to delay,
CC prevent or rescue retinal cells such as retinal neurons selected from
CC photoreceptors, retinal ganglion cells, displaced retinal ganglion
CC cells, amacrine cells, displaced amacrine cells, horizontal and
CC bipolar neurons, and supportive cells (including Mueller cells and
CC pigment epithelial cells) from injury and degradation. The retinal
CC cells are preferably photoreceptors and photoreceptor cell injury or
CC death is caused by retinal injury, light or environmental trauma or
CC by an ocular disease selected from retinitis pigmentosa, macular
CC degeneration, including age-related, retinal detachment, retinal
CC tears, retinopathy, retinal degenerative diseases, macular holes,
CC degenerative myopia, acute retinal necrosis syndrome, traumatic
CC chorioretinopathies or contusion such as Purtscher's retinopathy,
CC edema, ischemic conditions such as central or branch retinal vision
CC occlusion, collagen vascular diseases, thrombocytopenic purpura,
CC uveitis, retinal vasculitis and occlusion associated with Bales

CC disease and systemic lupus erythematosus (claimed).

XX
SQ Sequence 345 AA;
Query Match 99.6%; Score 1851; DB 21; Length 345;
Best Local Similarity 99.4%; Pred. No. 7e-179; Mismatches 0; Indels 0; Gaps 0;
Matches 343; Conservative 2;
QY 1 MSFLGGLLVTSALAGQRRGTAESNLSSKTFSSKKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MSFLGGLLVTSALAGQRRGTAESNLSSKTFSSKKEQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHPTVPRNTLVWRVLAIVENWVQLTDERFGLDEPDDEICKYDFVEEPEPSDGTIL 120
DB 61 PRPHPTVPRNTLVWRVLAIVENWVQLTDERFGLDEPDDEICKYDFVEEPEPSDGTIL 120
QY 121 GRWCGSTVPGKQISKGNQIRIRVSDYPPSEPGFCIHYNVMPQTEAVPSVLPPSA 180
DB 121 GRWCGSTVPGKQISKGNQIRIRVSDYPPSEPGFCIHYNVMPQTEAVPSVLPPSA 180
QY 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240
DB 181 LPDLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240
QY 241 LTBVRLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNEQCVPFSK 300
DB 241 LTBVRLYSCTPRNFVSIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNEQCVPFSK 300
QY 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEHEDCVCGRSTGG 345
DB 301 VTKKYHEVLQRPKTGVRGLHKSITDVALEHHEHEDCVCGRSTGG 345

RESULT 15
AAB33414
ID AAB33414 standard; Protein; 345 AA.
AC AAB33414;

XX
XX 29-JAN-2001 (first entry)

XX
XX Human PRO200 protein UNQ174 SEQ ID NO:2.

XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatologic; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; neutrotropic; neuroprotective;
KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.

OS Homo sapiens.

XX
XX WC2000053758-A2.

XX
XX 14-SEP-2000.

XX
XX 02-MAR-2000; 2000WO-US05841.

XX
XX 08-MAR-1999; 99WO-US05028.

PR
PR 10-MAR-1999; 99US-0123618.

PR
PR 12-MAR-1999; 99US-0123957.

PR
PR 23-MAR-1999; 99US-0125775.

PR
PR 12-APR-1999; 99US-0128849.

PR
PR 20-APR-1999; 99WO-US08615.

PR
PR 28-APR-1999; 99US-0131445.

PR 04-MAY-1999; 99US-0132371.
PR 14-MAY-1999; 99US-0134287.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-OCT-1999; 99US-0162506.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 11-FEB-2000; 2000WO-US00376.
PR 18-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.

(GETH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Fan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX WPI; 2000-572271/53.

DR N-PSDB; AAC58579.
XX

PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
PS Claim 33; Fig 2; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, thyroiditis, diabetes mellitus,
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central
CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
CC autoimmune or immune-mediated skin diseases, allergic diseases,
CC immunological diseases of the lung, and transplantation associated
CC diseases including graft rejection and graft-versus-host-disease.
CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.

SQ Sequence 345 AA;

Query Match

Best Local Similarity 99.4%; Score 1851; DB 21; Length 345;

Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 21:04:39 ; Search time 24.3006 Seconds
(without alignments)
2618.575 Million cell updates/sec

Title: US-09-852-209A-3

Perfect score: 1858

Sequence: 1 MSFGLLLVTSALAGQRGT.....DVALEHHECDVCVRGSGTG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 18443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	1858	100.0	345	9	US-09-818-943-1
2	1858	100.0	345	10	US-09-852-209A-3
3	1858	100.0	345	14	US-10-086-623-32
4	1858	100.0	345	15	US-10-260-539-32
5	1858	100.0	345	15	US-10-431-600-3
6	1851	99.6	345	9	US-09-823-033-2
7	1851	99.6	345	9	US-09-923-995-4
8	1851	99.6	345	10	US-09-795-006A-149
9	1851	99.6	345	10	US-09-978-295A-488
10	1851	99.6	345	10	US-09-978-697-488
11	1851	99.6	345	10	US-09-978-192A-488
12	1851	99.6	345	10	US-09-999-832A-488
13	1851	99.6	345	11	US-09-978-189-488
14	1851	99.6	345	11	US-09-796-753-6
15	1851	99.6	345	11	US-09-978-608A-488

16	1851	99.6	345	11	US-09-978-585A-488	Sequence 488, App
17	1851	99.6	345	11	US-09-978-191A-488	Sequence 488, App
18	1851	99.6	345	11	US-09-978-403A-488	Sequence 488, App
19	1851	99.6	345	11	US-09-978-564A-488	Sequence 488, App
20	1851	99.6	345	11	US-09-999-833A-488	Sequence 488, App
21	1851	99.6	345	11	US-09-981-915A-488	Sequence 488, App
22	1851	99.6	345	11	US-09-978-824-488	Sequence 488, App
23	1851	99.6	345	11	US-09-918-585A-488	Sequence 488, App
24	1851	99.6	345	11	US-09-978-423A-488	Sequence 488, App
25	1851	99.6	345	11	US-09-978-193A-488	Sequence 488, App
26	1851	99.6	345	11	US-09-999-830A-488	Sequence 488, App
27	1851	99.6	345	11	US-09-978-757A-488	Sequence 488, App
28	1851	99.6	345	11	US-09-978-187B-488	Sequence 488, App
29	1851	99.6	345	11	US-09-978-643A-488	Sequence 488, App
30	1851	99.6	345	12	US-09-978-375A-488	Sequence 488, App
31	1851	99.6	345	12	US-09-978-188A-488	Sequence 488, App
32	1851	99.6	345	12	US-09-978-298A-488	Sequence 488, App
33	1851	99.6	345	12	US-10-137-870-286	Sequence 286, App
34	1851	99.6	345	12	US-10-140-018-286	Sequence 286, App
35	1851	99.6	345	12	US-10-140-021-286	Sequence 286, App
36	1851	99.6	345	12	US-10-140-274-286	Sequence 286, App
37	1851	99.6	345	12	US-10-140-471-286	Sequence 286, App
38	1851	99.6	345	12	US-10-140-807-286	Sequence 286, App
39	1851	99.6	345	12	US-10-140-922-286	Sequence 286, App
40	1851	99.6	345	12	US-10-140-924-286	Sequence 286, App
41	1851	99.6	345	12	US-10-141-698-286	Sequence 286, App
42	1851	99.6	345	12	US-10-141-702-286	Sequence 286, App
43	1851	99.6	345	12	US-10-141-704-286	Sequence 286, App
44	1851	99.6	345	12	US-10-142-421-286	Sequence 286, App
45	1851	99.6	345	12	US-10-142-421-286	Sequence 286, App

ALIGNMENTS

RESULT 1

US-09-818-943-1
; Sequence 1, Application US/09818943
; Patent No. US20020049987A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: LI, Xuri
; APPLICANT: FONTEN, Annica
; APPLICANT: AASE, Karin
; APPLICANT: LI, Hong
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH
; FILE REFERENCE: 1064/48487
; CURRENT APPLICATION NUMBER: US/09/818,943
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,507
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-818-943-1

Query Match 100.0%; Score 1858; DB 9; Length 345;

Best Local Similarity 100.0%; Pred. No. 3.1e-179;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSFGLLLVTSALAGQRGTQAESNLSSKQFSSNKQNGVQDPQHERIIIVTNGSIHS 60

Db 1 MSFGLLLVTSALAGQRGTQAESNLSSKQFSSNKQNGVQDPQHERIIIVTNGSIHS 60

Qy 61 PRFHTYPRNTLVWRLVAEENVWIIQLTDFERGLEDPEDDICKYDFVEEPESDGITL 120

Db 61 PRFHTYPRNTLVWRLVAEENVWIIQLTDFERGLEDPEDDICKYDFVEEPESDGITL 120

Qy 121 GRWCGSTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHVNVMPQFTEAVSPSLPPSA 180

Db 121 GRWCGSGTVPKQISKGNQIRIRFVSDYFPPSEPGFCIHYNVMPQTEAVSPSVLPSPA 180
Qy 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240
Db 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240
Qy 241 LTEEVLVYSCYTPRNFVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Db 241 LTEEVLVYSCYTPRNFVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Qy 301 VTKKYHEVLQRPKTGVRGLHKSLLTDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTGVRGLHKSLLTDVALEHHEECDCVCRGSTGG 345

RESULT 2

US-09-852-209A-3
; Sequence 3, Application US/09852209A
; Patent No. US20020164687A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETHSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/09/852,209A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-209A-3

Query Match 100.0%; Score 1858; DB 10; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.1e-179;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MSLFGLLVTSALAGQRRGTQAESNLSSKFPSSNKQNGVQDPQHERIITVSTNGSIHS 60
Qy 61 PRPHTYPRNTVLVWRLVAEENVMQITFDFRFGLEDDEDDICKYDFVEVEEPPSDGTIL 120
Db 61 PRPHTYPRNTVLVWRLVAEENVMQITFDFRFGLEDDEDDICKYDFVEVEEPPSDGTIL 120
Qy 121 GRWCGSGTVPKQISKGNQIRIRFVSDYFPPSEPGFCIHYNVMPQTEAVSPSVLPSPA 180
Db 121 GRWCGSGTVPKQISKGNQIRIRFVSDYFPPSEPGFCIHYNVMPQTEAVSPSVLPSPA 180
Qy 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240
Db 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240

Qy 241 LTEEVLVYSCYTPRNFVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Db 241 LTEEVLVYSCYTPRNFVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Qy 301 VTKKYHEVLQRPKTGVRGLHKSLLTDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRPKTGVRGLHKSLLTDVALEHHEECDCVCRGSTGG 345

RESULT 3

US-10-086-623-32
; Sequence 32, Application US/10086623
; Publication No. US20020164710A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/086,623
; CURRENT FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Amino acid sequence for PDGF-C
US-10-086-623-32

Query Match 100.0%; Score 1858; DB 14; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.1e-179;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MSLFGLLVTSALAGQRRGTQAESNLSSKFPSSNKQNGVQDPQHERIITVSTNGSIHS 60
Qy 61 PRPHTYPRNTVLVWRLVAEENVMQITFDFRFGLEDDEDDICKYDFVEVEEPPSDGTIL 120
Db 61 PRPHTYPRNTVLVWRLVAEENVMQITFDFRFGLEDDEDDICKYDFVEVEEPPSDGTIL 120
Qy 121 GRWCGSGTVPKQISKGNQIRIRFVSDYFPPSEPGFCIHYNVMPQTEAVSPSVLPSPA 180
Db 121 GRWCGSGTVPKQISKGNQIRIRFVSDYFPPSEPGFCIHYNVMPQTEAVSPSVLPSPA 180
Qy 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240
Db 181 LPDLNNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240
Qy 241 LTEEVLVYSCYTPRNFVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300

Db 241 LTEVRVLYSCTPRNFSVSIIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
QY 301 VTKKYHEVLQRLPKTGVGRGLHKSITDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRLPKTGVGRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 4
US-10-260-539-32
; Sequence 32, Application US/10260539
; Publication No. US20030073637A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES THEREOF
; FILE REFERENCE: 1064/44833C2
; CURRENT APPLICATION NUMBER: US/10/260,539
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US/10/086,623
; PRIOR FILING DATE: 2000-03-04
; PRIOR APPLICATION NUMBER: US 60/107,852
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 60/113,997
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: US 60/150,604
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: US 60/157,108
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: US 60/157,756
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 09/438,046
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 09/691,200
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Amino acid sequence for PDGF-C
US-10-260-539-32

Query Match 100.0%; Score 1858; DB 15; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.1e-179;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLVTSALAQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Db 1 MSLFGLLVTSALAQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60

QY 61 PRPPTYPRNTVLVWRLVAEENWVQLTDFRFGLEDPEDDI CKYDFVEVEEPSDGTIL 120
Db 61 PRPPTYPRNTVLVWRLVAEENWVQLTDFRFGLEDPEDDI CKYDFVEVEEPSDGTIL 120

QY 121 GRWCSGTVPGQISKGNQIRIRFVSDVEYFPSEPGFCHYINVMQFTEAVSPSVLPSPA 180
Db 121 GRWCSGTVPGQISKGNQIRIRFVSDVEYFPSEPGFCHYINVMQFTEAVSPSVLPSPA 180

QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDYRPTWQLLGKAFVFGKSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDYRPTWQLLGKAFVFGKSRVVDLNL 240

QY 241 LTEVRVLYSCTPRNFSVSIIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Db 241 LTEVRVLYSCTPRNFSVSIIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300

Db 241 LTEVRVLYSCTPRNFSVSIIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
QY 301 VTKKYHEVLQRLPKTGVGRGLHKSITDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRLPKTGVGRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 5
US-10-131-600-3
; Sequence 3, Application US/10131600
; Publication No. US20030082670A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING THEREFOR, AND USES THEREOF
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/10/131,600
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-600-3

Query Match 100.0%; Score 1858; DB 15; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.1e-179;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLFGLLVTSALAQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Db 1 MSLFGLLVTSALAQRRGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60

QY 61 PRPPTYPRNTVLVWRLVAEENWVQLTDFRFGLEDPEDDI CKYDFVEVEEPSDGTIL 120
Db 61 PRPPTYPRNTVLVWRLVAEENWVQLTDFRFGLEDPEDDI CKYDFVEVEEPSDGTIL 120

QY 121 GRWCSGTVPGQISKGNQIRIRFVSDVEYFPSEPGFCHYINVMQFTEAVSPSVLPSPA 180
Db 121 GRWCSGTVPGQISKGNQIRIRFVSDVEYFPSEPGFCHYINVMQFTEAVSPSVLPSPA 180

QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDYRPTWQLLGKAFVFGKSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDYRPTWQLLGKAFVFGKSRVVDLNL 240

QY 241 LTEVRVLYSCTPRNFSVSIIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Db 241 LTEVRVLYSCTPRNFSVSIIRBELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300

QY 301 VTKKYHEVLQRLPKTGVGRGLHKSITDVALEHHEECDCVCRGSTGG 345
Db 301 VTKKYHEVLQRLPKTGVGRGLHKSITDVALEHHEECDCVCRGSTGG 345

RESULT 6
US-09-823-033-2
; Sequence 2, Application US/09823033
; Patent No. US2002004225A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-033-2

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSLFGLLLVTSALAGORGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Qy 61 PRFPHYTPRNTVLVWRLVAEENWVWQLTDFERFGLDEPDIDICKYDFVEVEEPSDGTIL 120
Db 61 PRFPHYTPRNTVLVWRLVAEENWVWQLTDFERFGLDEPDIDICKYDFVEVEEPSDGTIL 120
Qy 121 GRWCGSGTVPGKQISKNQIRIRFVSDYFPEPFCIHYNVMPQFTVAVSPSVLPSSA 180
Db 121 GRWCGSGTVPGKQISKNQIRIRFVSDYFPEPFCIHYNVMPQFTVAVSPSVLPSSA 180
Qy 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWLLGKAFVFGKRSRVVDLNL 240
Qy 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Qy 301 VTKKYHEVLQRLPKTGVRGLHKS LTDVALEHHEECDCVCRGSTG 345
Db 301 VTKKYHEVLQRLPKTGVRGLHKS LTDVALEHHEECDCVCRGSTG 345
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Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
US-09-923-995-4
; Sequence 4, Application US/09923995
; Patent No. US20020081700A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNKI
; FILE REFERENCE: 00-47
; CURRENT APPLICATION NUMBER: US/09/923,995
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,164
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-995-4

Query Match 99.6%; Score 1851; DB 9; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-178;

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Qy 1 MSLFGLLLVTSALAGORGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Qy 61 PRFPHYTPRNTVLVWRLVAEENWVWQLTDFERFGLDEPDIDICKYDFVEVEEPSDGTIL 120
Db 61 PRFPHYTPRNTVLVWRLVAEENWVWQLTDFERFGLDEPDIDICKYDFVEVEEPSDGTIL 120
Qy 121 GRWCGSGTVPGKQISKNQIRIRFVSDYFPEPFCIHYNVMPQFTVAVSPSVLPSSA 180
Db 121 GRWCGSGTVPGKQISKNQIRIRFVSDYFPEPFCIHYNVMPQFTVAVSPSVLPSSA 180
Qy 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWLLGKAFVFGKRSRVVDLNL 240
Qy 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Qy 301 VTKKYHEVLQRLPKTGVRGLHKS LTDVALEHHEECDCVCRGSTG 345
Db 301 VTKKYHEVLQRLPKTGVRGLHKS LTDVALEHHEECDCVCRGSTG 345
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RESULT 8

US-09-795-006A-149
; Sequence 149, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 149
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-006A-149

Query Match 99.6%; Score 1851; DB 10; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MSLFGLLLVTSALAGORGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Db 1 MSLFGLLLVTSALAGORGTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Qy 61 PRFPHYTPRNTVLVWRLVAEENWVWQLTDFERFGLDEPDIDICKYDFVEVEEPSDGTIL 120
Db 61 PRFPHYTPRNTVLVWRLVAEENWVWQLTDFERFGLDEPDIDICKYDFVEVEEPSDGTIL 120
Qy 121 GRWCGSGTVPGKQISKNQIRIRFVSDYFPEPFCIHYNVMPQFTVAVSPSVLPSSA 180
Db 121 GRWCGSGTVPGKQISKNQIRIRFVSDYFPEPFCIHYNVMPQFTVAVSPSVLPSSA 180
Qy 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWLLGKAFVFGKRSRVVDLNL 240
Db 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWLLGKAFVFGKRSRVVDLNL 240
Qy 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Db 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
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QY 301 VTKKYHEVLQLRPKTGVRLHKSLTDVALEHHEECDVCRGSTGG 345
|||
Db 301 VTKKYHEVLQLRPKTGVRLHKSLTDVALEHHEECDVCRGSTGG 345

RES. 11. T. 9

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US-09-378-295A-488
? Sequence 488, Application US/09978295A
? Patent No. US2002015606A1
? GENERAL INFORMATION:
? APPLICANT: Ashkenazi, Avi
? APPLICANT: Baker Kevin P.
? APPLICANT: Botstein, David
? APPLICANT: Desnoyers, Luc
? APPLICANT: Eaton, Dan
? APPLICANT: Ferrara, Napoleon
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Fong, Sherman
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Gerber, Hanspeter
? APPLICANT: Gerritsen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Gurney, Austin L.
? APPLICANT: Hillan, Kenneth J.
? APPLICANT: Kljavin, Ivar J.
? APPLICANT: Kuo, Sophia S.
? APPLICANT: Napier, Mary A.
? APPLICANT: Pan, James;
? APPLICANT: Paoni, Nicholas F.
? APPLICANT: Roy, Margaret Ann
? APPLICANT: Shelton, David L.
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tamas, Daniel
? APPLICANT: Williams, P. Mickey
? APPLICANT: Wood, William L.
? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
? ACIDS Encoding the Same
? FILE REFERENCE: P2630P1C11
? CURRENT APPLICATION NUMBER: US/09/978,295A
? CURRENT FILING DATE: 2001-10-15
? PRIOR APPLICATION NUMBER: 09/918585
? PRIOR FILING DATE: 2001-07-30
? PRIOR APPLICATION NUMBER: 60/062250
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/064249
? PRIOR FILING DATE: 1997-11-03
? PRIOR APPLICATION NUMBER: 60/065311
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? PRIOR APPLICATION NUMBER: 60/066364
? PRIOR FILING DATE: 1997-11-21
? PRIOR APPLICATION NUMBER: 60/077450
? PRIOR FILING DATE: 1998-03-10
? PRIOR APPLICATION NUMBER: 60/077632
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? PRIOR APPLICATION NUMBER: 60/077641
? PRIOR FILING DATE: 1998-03-11
? PRIOR APPLICATION NUMBER: 60/077649
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? PRIOR APPLICATION NUMBER: 60/077791
? PRIOR FILING DATE: 1998-03-12
? PRIOR APPLICATION NUMBER: 60/078004
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? PRIOR APPLICATION NUMBER: 60/078886
? PRIOR FILING DATE: 1998-03-20
? PRIOR APPLICATION NUMBER: 60/078936
? PRIOR FILING DATE: 1998-03-20
? PRIOR APPLICATION NUMBER: 60/078910
? PRIOR FILING DATE: 1998-03-20
? PRIOR APPLICATION NUMBER: 60/078939
? PRIOR FILING DATE: 1998-03-20

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[illegible]


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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match          99.6%; Score 1851; DB 10; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFLGLLVTSALAGORGTQAEENLSKQFSSKQNGVQDPQDQHRITITVSTNGSIHS 60
Db 1 MSFLGLLVTSALAGORGTQAEENLSKQFSSKQNGVQDPQDQHRITITVSTNGSIHS 60
QY 61 PRFHTYPRNTVLYWRLVAVENWVQITQDERGLEDEPDIDCKYDFVEVEPSDGTIL 120
Db 61 PRFHTYPRNTVLYWRLVAVENWVQITQDERGLEDEPDIDCKYDFVEVEPSDGTIL 120
QY 121 GRWCGSTVPKGQISKGNQIRIRFVSDRYFPSEFGFCHYINVMQFTEAVSPSVLPSSA 180
Db 121 GRWCGSTVPKGQISKGNQIRIRFVSDRYFPSEFGFCHYINVMQFTEAVSPSVLPSSA 180
QY 181 LPDLNLNNAITAFSTLEDLIRYLPERWQDLEDLRYPTWQLLCKAFVFGKRSVVDLNL 240
Db 181 LPDLNLNNAITAFSTLEDLIRYLPERWQDLEDLRYPTWQLLCKAFVFGKRSVVDLNL 240
QY 241 LTEEVRVLYSCPTNPFVSIRBELKRTDTIFWPFGCLLVKRCGNCACCLHNCNECCQVPSK 300
Db 241 LTEEVRVLYSCPTNPFVSIRBELKRTDTIFWPFGCLLVKRCGNCACCLHNCNECCQVPSK 300
QY 301 VTKKYHEVLQRPKTVGLHLSLTDVALEHHERCDVCRCSTGG 345
Db 301 VTKKYHEVLQRPKTVGLHLSLTDVALEHHERCDVCRCSTGG 345

RESULT 11
US-09-978-192A-488
; Sequence 488, Application US/09978192A
; Patent No. US2002017553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tuma, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC9
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US/09/978,192A
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
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; PRIOR FILING DATE: 1998-05-13

; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match          99.6%; Score 1851; DB 10; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFGLLLVTSALAGORGTQAESNLSSKFPQSSNKEQNGVDPQHERIITVSTNGSIHS 60
Db 1 MSFGLLLVTSALAGORGTQAESNLSSKFPQSSNKEQNGVDPQHERIITVSTNGSIHS 60
QY 61 PRFPHTYPRNTVLVWRLVAEENVWIQLTFDERFGLDEPDDICKYDFVEVEPSDGTIL 120
Db 61 PRFPHTYPRNTVLVWRLVAEENVWIQLTFDERFGLDEPDDICKYDFVEVEPSDGTIL 120
QY 121 GRWCGSGTVGKQISKGNQIRIRFVSDEYFPPSPGFCIHNIYVMPQFTEAVSPSVLPSSA 180
Db 121 GRWCGSGTVGKQISKGNQIRIRFVSDEYFPPSPGFCIHNIYVMPQFTEAVSPSVLPSSA 180
QY 181 LPDLNNNAITAFSTLEDLIRYLEPERWOLDLEDLIRPTWOLLGKAFVFGKSRVVDLNL 240
Db 181 LPDLNNNAITAFSTLEDLIRYLEPERWOLDLEDLIRPTWOLLGKAFVFGKSRVVDLNL 240
QY 241 LTBVRLYSCTPRNFVSIREELKRTDTIPWPGCLLVKRCGGNCACCLHNCNCCQVPSK 300
Db 241 LTBVRLYSCTPRNFVSIREELKRTDTIPWPGCLLVKRCGGNCACCLHNCNCCQVPSK 300
QY 301 VTKKYEVLQLRPKTVGRGLHKSILTDALEHHEECDCVCRGSGTG 345
Db 301 VTKKYEVLQLRPKTVGRGLHKSILTDALEHHEECDCVCRGSGTG 345

RESULT 12
US-09-999-832A-488
; Sequence 488, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
```

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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;; PRIOR FILING DATE: 1998-05-15
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Query Match 99.6%; Score 1851; DB 10; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFLGLLVTALAGORGTQAESNLSSKFOFSSNKQGVQDPQHERIIIVTNGSIHS 60
DB 1 MSFLGLLVTALAGORGTQAESNLSSKFOFSSNKQGVQDPQHERIIIVTNGSIHS 60
QY 61 PRFPHTYPRNTLVWRLVAEENWVIQLTDFERFGLDEPDDICKYDFVEVEEFSDDGTL 120
DB 61 PRFPHTYPRNTLVWRLVAEENWVIQLTDFERFGLDEPDDICKYDFVEVEEFSDDGTL 120
QY 121 GRWCGSGTVPGKQISGKNQIRIRFVSDYFEPSEPGFCIHYINVMPQFTEAVSPVLPPSA 180
DB 121 GRWCGSGTVPGKQISGKNQIRIRFVSDYFEPSEPGFCIHYINVMPQFTEAVSPVLPPSA 180
QY 181 LPDLILNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWOLLGKAFVFGKRSRVDLNL 240
DB 181 LPDLILNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWOLLGKAFVFGKRSRVDLNL 240
QY 241 LTEEVRVLYSCTPRNFSVSIREEBKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
DB 241 LTEEVRVLYSCTPRNFSVSIREEBKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
QY 301 VTKKYHEVLQRPKTVGRLGKSLTDVALRHEEEDCDVCRGSGTG 345
DB 301 VTKKYHEVLQRPKTVGRLGKSLTDVALRHEEEDCDVCRGSGTG 345

RESULT 13

US-09-978-189-488
; Sequence 488, Application US/09978189
; GENERAL INFORMATION:
; Publication No. US20030004102A1
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630PIC7
;; CURRENT APPLICATION NUMBER: US/09/978,189
;; CURRENT FILING DATE: 2001-10-15
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;; PRIOR FILING DATE: 2001-07-30
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Query Match 99.6%; Score 1851; DB 11; Length 345;
Best Local Similarity 99.4%; Pred. No. 1.6e-178;
Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLLVTSALAGRGRTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Db 1 MSIFGLLLVTSALAGRGRTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHTYPRNTVLVWRLVAVEENVWVQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
Db 61 PRPHTYPRNTVLVWRLVAVEENVWVQLTFDERFGLDEPDDICKYDFVEVEEPSDGTIL 120
QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFPPSPGFCIHYNIVMPQTEAVSFLPSPA 180
Db 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFPPSPGFCIHYNIVMPQTEAVSFLPSPA 180
QY 181 LPDLNNNAITAFSTLLEDLIRYLEPERWQJLDLEDLIRPTWQLLGKAFVFGKRVRVDNL 240
Db 181 LPDLNNNAITAFSTLLEDLIRYLEPERWQJLDLEDLIRPTWQLLGKAFVFGKRVRVDNL 240
QY 241 LVEEVLVYCTPRNFVSIRREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNCCQVPSK 300
Db 241 LVEEVLVYCTPRNFVSIRREELKRTDTTFWPGCLLVKRCGGNCACCLHNCNCCQVPSK 300
QY 301 VTKKXHEVLQLRPKTGVRGLHKSLLTDVALEHHEECDCVCRGSGTG 345
Db 301 VTKKXHEVLQLRPKTGVRGLHKSLLTDVALEHHEECDCVCRGSGTG 345


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Db      1  MSUFGLLLSALAGQQTQAESNLSSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
Qy      61  PRFPHYPRNTVLVWRLVAVENWMIQLTFDERFGLBDEDDICKYDFVEVEEPPSDGTIL 120
Db      61  PRFPHYPRNTVLVWRLVAVENWMIQLTFDERFGLBDEDDICKYDFVEVEEPPSDGTIL 120
Qy     121  GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPEFPGFCIHYNIVMPQFTEAVSPSVLPSSA 180
Db     121  GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPEFPGFCIHYNIVMPQFTEAVSPSVLPSSA 180
Qy     181  LPLDLLNNAITAPSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDNL 240
Db     181  LPLDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDNL 240
Qy     241  LTEEVRLYSCTPRNFSYSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Db     241  LTEEVRLYSCTPRNFSYSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
Qy     301  VTKKYHEVLQIRPKTGVRLHKSITDVALEHHEECDCVCRGSTGG 345
Db     301  VTKKYHEVLQIRPKTGVRLHKSITDVALEHHEECDCVCRGSTGG 345
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Search completed: November 25, 2003, 21:17:04
Job time : 25.3006 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:59:34 ; Search time 14.7173 Seconds
(without alignments)
2254.373 Million cell updates/sec

Title: US-09-852-209A-3

Perfect score: 1858

Sequence: 1 MSLFGLLVTSALAGQRRGT.....DVALEHHEEDCVCKGSGTGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: piri:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	742.5	40.0	370	JC7591	spinal cord-derive
2	736	39.6	370	JC7592	spinal cord-derive
3	183	9.8	3623	T09456	intrinsic factor-B
4	181.5	9.8	730	BMH1	procollagen C-endo
5	179.5	9.7	927	JQ0948	A5 antigen precurs
6	176	9.5	707	JC2218	procollagen C-endo
7	176	9.5	3623	T08618	intrinsic factor-B
8	173	9.3	823	A58788	procollagen C-endo
9	169	9.1	986	B58788	procollagen C-endo
10	169	9.1	991	I49540	procollagen C-endo
11	154	8.3	449	A55362	procollagen I C-pr
12	148.5	8.0	1057	A39288	dorsal-ventral pat
13	143.5	7.7	686	A59271	Ra-reactive factor
14	139.5	7.5	1070	T31069	colloid-BMP-I like
15	138.5	7.5	597	S71352	metalloproteinase
16	138	7.4	705	CIHURB	complement subcomp
17	137.5	7.4	699	I54763	Ra-reactive factor
18	137.5	7.4	1524	T30337	polyprotein - Afri
19	133	7.2	1594	T30549	hensin - rabbit
20	132	7.1	419	S69207	vascular endotheli
21	130.5	7.0	1464	S58984	development protei
22	128	6.9	402	JH0403	procollagen I C-pr
23	127.5	6.9	767	T30018	hypothetical prote
24	127.5	6.9	3871	T22812	hypothetical prote
25	125	6.7	198	J50735	platelet-derived g
26	123.5	6.6	277	A41735	hyaluronate-bindin
27	123.5	6.6	579	JC7629	membrane-type friz
28	120.5	6.5	245	1 TVC155	platelet-derived g
29	120.5	6.5	275	JC6506	tumor necrosis fac

ALIGNMENTS

RESULT 1

JC7591 spinal cord-derived growth factor-B precursor - human

C/Species: Homo sapiens (man)

C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001

C/Accession: JC7591

R/Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.

Biochem. Biophys. Res. Commun. 280, 733-737, 2001

A/Title: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-F; F18-370/Product: spinal cord-derived growth factor-B #status predicted

A/Reference number: JC7591; PMID:2102670; PMID:11162582

A/Accession: JC7591

A/Molecule type: DNA

A/Residues: 1-370 <HAM>

A/Cross-references: DDBJ:AB033832

C/Genetics:

A/Gene: scdgf-B

F1:17/Domain: secretory signal sequence #status predicted <SIG>

F18-370/Product: spinal cord-derived growth factor-B #status predicted <MFT>

F52-170/Region: CUB domain #status predicted

F272-370/Region: homologous to platelet-derived growth factor/vascular endothelial gr

F294-308/Region: conserved motif #status predicted

Query Match 40.0%; Score 742.5; DB 2; Length 370;

Best Local Similarity 43.6%; Pred. No. 9e-57;

Matches 159; Conservative 59; Mismatches 114; Indels 33; Gaps 10;

QY 3 LFGLLVTSALAGQRRGTQAESNLSSKFPQSSN---KEQNGVDP-PQHERIITVSTNGSI 58

Db 5 IFVYTLICANFSCSDTSATPQSNASIKALRNANLRRDESNNHLLDLYRRDETIOVKGNGYV 64

QY 59 HSPRPHTYPRNTVLVWRLVAENVWVQLTFDRFGLEDDEDDICKYDFVEVEPSDGT 118

Db 65 QSPRPFSYPRNLLLTWRHLS-QENTRIQLVFNQFGLAEANDICKYDFVEVEDISETS 123

QY 119 --IIGRWCGSTVPGKQISGNQIRIFVSDVFPSPGFCIHVNIWMPQTEAV----- 171

Db 124 TIIRKRWGCHKEVPPRIKSRNQIKITFKSDDTFVAPRGKIYSL-LEDPQAASETN 182

QY 172 -----SPSLPPSALPLDLNNAITAFSTLEDLIRYLEPERWQDLEDLYR 217

Db 183 WESVTSISGVSYNPSVTDPT-LIADALOKIAEPTVEDLLKYFNPESQWEDLENNYL 241

QY 218 PTWQLLGKAFVGRKSRVDNLNLTTEVRLYSCSTPRNFSVIREELKRTDTIWPQCLLV 277

Db 242 DTPYRGSRV-HSRKSK-VLDRLNDADKRYSTPRNYSVIREELKLANVWFFPCLLV 299

QY 278 KRCCGNCACCHNCNECCQVPSKVTKYHEVQLQRP---KTGVRGLHKSITDVALEHHEE 334

Db 300 QRCGNGCGCTVNRWSTCNSGKTVKYYHEVQLQFPGHKRRGRKAKTMAVLDQLDHER 359

QY 335 CDCVC 339

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Gene 134, 257-261., 1993

A;Title: Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic protein
A;Reference number: J02218; MUID:94085787; PMID:8262384

A;Accession: J02218

A:Molecule type: mRNA

A:Residues: 1-707 <NAE>

A:Cross-references: L12249; NID:g406540; PIDN:AAA16133.1.; PID:g406541

C;Comment: This protein induces ectopic cartilage formation in vivo.

C;Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology;
C;Keywords: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc

F/g3-284/Domain: astacin homology <AST>

F/285-397/Region: complement 1r/1s-like repeat

F/285-394/Domain: Clr/Cls repeat homology <CLR1>

F/398-510/Region: complement 1r/1s-like repeat

F/398-507/Domain: Clr/Cls repeat homology <CLR2>

F/514-550/Domain: EGF homology <EGF>

F/554-666/Region: complement 1r/1s-like repeat

F/554-663/Domain: Clr/Cls repeat homology <CLR3>

F/62,105,295,326/Binding site: carbohydurate (Asn) (covalent) #status predicted

F/176,180,186,235/Binding site: zinc (His, His, His, Tyr) #status predicted

F/177/Active site: Glu #status predicted

F/528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 9.5%; Score 176; DB 2; Length 707;
Best Local Similarity 43.3%; Pred.No. 4.2e-07;
Matches 45; Conservative 15; Mismatches 36; Indels 8; Gaps 5;

QY 55 NGSIHSFRPHPTVNTVLVRLVAENVVIQLTFDERGLEDPEDDICKYDFVEVEE- 113
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Db 562 NSGINSFGWPEYPNNKNCIMQLVAPIQ-YRISLKFDQ---PTEGNVDCKYDFVEVRSG 617
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QY 114 -PSDTGITLRCWGSGTVPGRKOISKGNQIRIRFSVDYEPPSPGGF 156
 ::::::::::::||:::||:::||:::||:::||:::||
Db 618 LTSCLKHGFCGS-ELPAVITSYNMNRIFPKSDNTV-SKKGF 659
 ::::::::::::||:::||:::||:::||:::||:::||

RESULT 7

T08618

I;Name: intrinsic factor-B12 receptor CUBILIN precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Aug-2002

C;Accession: T08618

R/Moestrup, S.K.; Koyrakci, R.; Kristiansen, M.; Kayesen, J.H.; Rasmussen, H.H.; Brault
J. Biol. Chem. 273, 5235-5242, 1998

A;Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies

A;Reference number: Z16459; MUID:98148073; PMID:9478979

A;Accession: T08618

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-3623 <MOE>

A:Cross-references: EMML:AFO22247; NID:g3834379; PIDN:AACT71661.1.; PID:g3834380

C Genetics:

A:Gene: CUBILIN

C/Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology

C/Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane

F/1-20/Domain: signal sequence #status predicted <SIG>

F/21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>

F/133-164/Domain: EGF homology <EGF1>

F/436-467/Domain: EGF homology <EGF>

Query Match 9.5%; Score 176; DB 2; Length 3623;
Best Local Similarity 25.5%; Pred.No. 3.3e-06;
Matches 95; Conservative 52; Mismatches 133; Indels 92; Gaps 24;

QY 2 SLFGLLIIVT--SALAGQRRTGAESNLSSKFQFNKNKGNGVQDPQHREKIIVTSNGSH 59
 ::::||:::||:::||:::||:::||:::||:::||:::||:::||:
Db 901 SVVNILVTVFVKSSSMENRGFTA-----KFSSDKLECG-----EVLTAST-GIIE 944
 ::::||:::||:::||:::||:::||:::||:::||:::||:::||:

QY 60 SPREFPHYBNTVLVRLVAENVWIQLTFDERGLEDPEDDICKYDFVEVEESPDDGTII 119
 ::::||:::||:::||:::||:::||:::||:::||:::||:::||:
Db 945 SPGHNPVPGNVCTWHVV-VORGLRIKLRFSS-FYLEFHYN--CTNDLYEIYDAQAQTFF 1000
 ::::||:::||:::||:::||:::||:::||:::||:::||:::||:

QY 120 LGRWCSGSTVPRKQISKGNQIRIRFSVDYEPPSEPGFTCHV-----NIVMQPFEAVSP 173
 ::::||:::||:::||:::||:::||:::||:::||:::||:::||:

Db	1001	LGRYCGK-SIPPSLTSMNSIKILTFVSDSALAHE-GFSINTEAIDASSVCLCYDTTFNFGM	1058
QY	174	SVLP-PSALPLDL-----LNNAI-----TAFSTLED-----LIRYLEPERWQLDLE	213
Db	1059	LSSPFNFNNPFSNWECIYITVGLNQOIALHFTDF-TLEDYFGSCQCVDFVE-----IR	1110
QY	214	DLYRPTWQLLGKAFVFGKSRVVDNLNLTVEEVLRY-----SCTPRNFVSISREELKRT	266
Db	1111	DGGVETSPVGG--IV--CGSVLPPTIISHSNKLWLKFKSDAALTAKGFSA-----	1156
QY	267	DTTFWPGCLLVKCGGNCACLLHNCNECQVPKSYKKIHE-----VLQLRPTKTVRGVLHKS	323
Db	1157	---YWDGS--STGCCGN-----LTTFGTGLTSPNYPMPYHSBCYMKLRASHG-SPFELE	1206
QY	324	LTDVALEHHBEC	335
Db	1207	FQDFHLEHHPSC	1218

RESULT 8

A58788

procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human

N;Alternate names: bone morphogenic protein splice form BMP-1/His

C;Species: Homo sapiens (man)

C;Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 18-Jun-1999

C;Accession: A37278; A58788

R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew Science 242, 1528-1534, 1998

A;Title: Novel regulators of bone formation: molecular clones and activities.

A;Reference number: A37278; MUID:99072730; PMID:3201241

A;Accession: A37278

A;Molecule type: mRNA

A;Residues: 1-702, *EKRPALQPPGRPHKFRVQKRNTPQ* <WOZ>

A;Cross-references: GB:M22488; NID:g179459; PIDN:AAA51833.1; PID:g179500

R;Takahara, K.; Lyons, G.E.; Greenspan, D.S. J. Biol. Chem. 269, 32572-32578, 1994

A;Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are encoded

A;Reference number: A58788; MUID:95096114; PMID:7798260

A;Accession: A58788

A;Molecule type: mRNA

A;Residues: 703-823 <TAK>

A;Cross-references: GB:L35278; NID:g619423; PIDN:AAC41703.1; PID:g619424

C;Genetics:

A;Gene: GDB:BMP1; BMP-1

A;Cross-references: GDB:125203; OMIM:112264

A;Map position: 8p21-8p21

C;Function:

A;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type

C;Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; F

C;Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl

F;1-22/Domain: signal sequence #status predicted <SIG>

F;73-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT>

F;130-321/Domain: astacin homology <AST>

F;322-431/Domain: C1r/C1s repeat homology <C1R1>

F;435-544/Domain: C1r/C1s repeat homology <C1R2>

F;551-587/Domain: EGF homology <EGF>

F;591-700/Domain: C1r/C1s repeat homology <C1R3>

F;738-752/Region: histidine-rich

F;91-142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;163-319,185-205,322-348,375-597,435-461,488-510,551-563,559-572,574-587,591-617,644-66

F;213,217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted

F;214/Active site: Glu #status predicted

F;565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

```
Query Match          9.3%; Score 173; DB 1; Length 823;  
Best Local Similarity 35.6%; Pred. No. 9.2e-07;  
Matches 52; Conservative 19; Mismatches 49; Indels 26; Gaps 7;  
  
QY   55 NGSIHSRPHPTYPNTVLVRLVA--VEENVWIIQLTDEREFLGDPEDDDICKYDFEVREE 113  
      :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db    599 NGSITSGWKPEYPPNKNCK:LQWLVAQTYSIQFDFETEG----NDVKCYDFEVRS 653
```

```

Qy 114 --PSDGTILRWCGSGTVPGKQISKGNOIRIRFVSDSEVPSPGRCIHNHVMQPTEAV 171
      :|::|||:|::|||:|::|||:|::|||:|::|||:|::|||:|::|||:|::|||:
Db 654 GLTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHPFSVLGAGDRH 711

Qy 172 S-----PSVL-----PPSAL 181
      |         |||
Db 712 SHLSGLBLLCPHALVDTPAPPASAL 737

RESULT 9
B58788
Procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - human
N;Alternate names: Bone morphogenic protein 1, tolloid-like splice form
C;Species: Homo sapiens (man)
C;Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 16-Jul-1999
A;Accession: A37278; B58788
R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; et al
Science 242, 1528-1534, 1988
A;Title: Novel regulators of bone formation: molecular clones and activities.
A;Reference number: A37278; PMID:89072730; PMID:3201241
A;Accession: A37278
A;Molecule type: mRNA
A;Residues: 1-702,'EKRPALPPRGPHQLKFRVKENRTPO' <WOZ>
A;Cross-references: GB:M22488; NID:9179499; PID:NAA51833.1; PID:gl79500
R;Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
A;Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mtld) are encod
A;Reference number: A58788; PMID:95096114; PMID:7798260
A;Accession: B58788
A;Molecule type: mRNA
A;Residues: 703-986 <TAK>
A;Cross-references: GB:L35279; NID:g6198860; PID:AAC41710.1; PID:g6198861
C;Genetics:
A;Gene: GDB:BMP1; BMP-1
A;Cross-references: GDB:I125203; OMIM:112264
A;Map position: bp21-8p21
C;Function:
A;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen tyros
C;Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology;
C;Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication;
F;1-22/Domain: signal sequence #status predicted <Sig>
F;23-986/Product: procollagen C-endopeptidase tolloid-like splice form #status predict
F;130-321/Domain: astacin homology <AST>
F;322-431/Domain: Clr/Cls repeat homology <Clr1>
F;435-544/Domain: Clr/Cls repeat homology <Clr2>
F;511-587/Domain: EGF homology <EG1>
F;591-700/Domain: Clr/Cls repeat homology <Clr3>
F;707-742/Domain: EGF homology <EG2>
F;747-856/Domain: Clr/Cls repeat homology <Clr4>
F;860-973/Domain: Clr/Cls repeat homology <Clr5>
F;91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-
F;213,217,223,272/Binding site: zinc (His, His, Tyr) #status predicted
F;214/Active site: Glu #status predicted
F;565,720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match          9.1%; Score 169; DB 1; Length 986;
Best Local Similarity 39.4%; Pred. No. 2.6e-06;
Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps 5;

Qy 55 NSGIHSFRPHTTYPRNTLVLRVA-VVENYWIQLTFDEREFGLEDPEDDICKYDFVEEE 113
      |||||:|::|||:|::|||:|::|||:|::|||:|::|||:|::|||:|::|||:
Db 599 NGSITSPGWKEYPFNKNCIWLAPQYRIQLQDFFEETEG----NDVCKYDFVEYS 653

Qy 114 --PSDGTILRWCGSGTVPGKQISKGNOIRIRFVSDSEVPSPGRCIHY 160
      :|::|||:|::|||:|::|||:|::|||:|::|||:|::|||:|::|||:
Db 654 GLTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 700

RESULT 10
I43540
Procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - mouse
C;Species: Mus musculus (house mouse)

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Db      224 AVSDSRRLKGFCD-APVGSISSEGNELLVQFVSDLSVTAD-GFSASYK-TLPRGTAKE 280
Qy      169 -----EAVSPSV-LPFSALP 182
        ||||| : |
Db      281 GQGPGPKRGTEPKVKLPFKSQP 302
        ||||| : |

RESULT 12
A39288
C:dorsal-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A39288
R:Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
Cell 67, 469-481, 1991
A>Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bone morphogenetic protein 1
A:Reference number: A39288; PMID:92034970; PMID:1840509
A:Accession: A39288
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1057 <SH>
A:CROSS-references: GB:M76976; NID:g157305; PIDN:AAA28491.1; PID:g157306
C:Genetics:
A:Gene: FlyBase:tld
A:CROSS-references: FlyBase:FBgn0003719
C:Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; C1r/C1s re-
C:Keywords: duplication; hydrolase; metalloproteinase; zinc
F:136-329/Domain: astacin homology <AST>
F:352-464/Domain: C1r/C1s repeat homology <Clr1>
F:468-578/Domain: C1r/C1s repeat homology <Clr2>
F:585-620/Domain: EGF homology <EG1>
F:624-740/Domain: C1r/C1s repeat homology <Clr3>
F:747-782/Domain: EGF homology <EG2>
F:787-896/Domain: C1r/C1s repeat homology <Clr4>
F:900-1013/Domain: C1r/C1s repeat homology <Clr5>
F:221,225,231,280/Binding site: zinc (His, His, His, Tyr) #status predicted
F:222/Active site: Glu #status predicted

Query Match          8.0%; Score 148.5; DB 1; Length 1057;
Best Local Similarity 38.0%; Pred. No. 0.00017;
Matches 38; Conservative 20; Mismatches 35; Indels 7; Gaps 5;

Qy      50 ITVTNGSIHSRPHTYPTNTVLWRLVAENVVIQLTFDERFGLEDPEDDICKYDFV 109
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      472 LKLTKDOSIDSFNTPMDYMPDKCVWRITA-PDNHQVALKF-QSFELE--KHGDCAYDFV 527
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy      110 EVEER-PSDGIILGRWCSGTVPGGKISKGNQIRRFVSVD 147
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      528 IIRGNHSDSLIGFCGDKLPPNIK-TFSNQMYIRFVSD 566
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 13
A59271
Ra-reactive factor (EC 3.4.21.-) 2 precursor - human
N:Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C:Species: Homo sapiens (man)
C>Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
C:Accession: A59271
R:Ethiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaible, W.J.; Laursen, S.B.; Poulsen, J.
Nature 386, 506-510, 1997
A>Title: A second serine protease associated with mannan-binding lectin that activates complement
A:Reference number: A59271; PMID:97242412; PMID:9087411
A:Accession: A59271
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-686 <JEN>
A:CROSS-references: GB:Y09926; NID:g4007626; PIDN:CAA71059.1; PID:g4007627
A:Experimental source: tissue liver
A>Note: submitted to GenBank, December 1996
A>Note: parts of this sequence, including the amino end of the mature protein, were deleted from the original submission
C:Genetics:
A:Gene: GDB:MASP2
A:CROSS-references: GDB:6071500

```

```

A:Map position: lp36.2-2-lp36.3
C:Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement factor H
C:Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine p
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F:19-134/Domain: C1r/C1s repeat homology <C1r1>
F:142-180/Domain: EGF homology <EGF>
F:184-293/Domain: C1r/C1s repeat homology <C1R2>
F:300-361/Domain: complement factor H repeat homology <FH1>
F:366-430/Domain: complement factor H repeat homology <FH2>
F:445-679/Domain: trypsin homology <TRY>
F:72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552,
F:158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:44-445/Cleavage site: Arg-Ile (autolytic) #status predicted
F:483,532,633/Active site: His, Asp, Ser #status predicted

Query Match          7.7%   Score 143.5;   DB 1;   Length 686;
Best Local Similarity 32.1%;   Pred. No. 0.00027;
Matches 34;   Conservative 25;   Mismatches 42;   Indels 5;   Gaps 4;

QY  55  NGSIHSPRPFTYPRNTVLVRLVAENVYVIQLTFDERFGLGDPEDDICKYDFVEVEEP 114
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   193  SGELSSPEYPRYPKLSSTCYIS-LSLEEGSVILDFVESFDVETHPTLCYDFLKIQ-- 249

QY  115  SDGTILORWCGSGTVPGKQISKGNQIRIRFVSDVEYFPSPGFCIH 160
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   250  TDREEHGFPGCGK-TLPHRIETKSNVTITVFVTOE-SDGHTGWKIH 293
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 14

T31069

tolloid-BMP-1 like protein 1 - California sea hare

N;Alternate names: Probable metalloprotease TBL-1

C;Species: *Aplysia californica* (California sea hare)

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 18-Aug-2000

C;Accession: T31069

R;Lit: Q.R.; Hattar, S.; Endo, S.; MacPhee, K.; Zhang, H.; Cleary, L.J.; Byrne, J.H.; Es

J. Neurosci. 17, 755-764, 1997

A;Title: A developmental gene (Tolloid/BMP-1) is regulated in *Aplysia* Neurons by treatment

A;Reference number: Z20965; PMID:98007484; PMID:8987797

A;Accession: T31069

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: mRNA

A;Residues: 1-1070 -LIU>

A;Cross-references: EMBL:U57369; NID:g1899041; PID:g1899042; PID:AAAC47485.1

C;Superfamily: Dorsal-ventral patterning protein colloid; astacin homology; C1r/C1s repeat

Query Match	7.5%;	Score 139.5;	DB 2;	Length 1070;
Best Local Similarity	21.9%;	Pred. No. 0.0011;		
Matches	70;	Conservative 36;	Mismatches 102;	Indels 111; Gaps 17;
QY	56	GSIHSPRFPHYTPRNTVLVWRLVAVENWVQL--TFERFGLDEPDDICKYDVEVVE	112	
Db	529	GLFNSPAYPDEYQSDKVCW-VITVREGVQVALEFATFTEF--DPD---CAYDIYEIR	581	
QY	113	--BPSGDTILGRWCWGSGTVPGKQISKGNQIRINFSVDEYFPSEPFGCIHY-----	160	
Db	582	DGDTKDSPLVGTYCGTRT-PPNAISTSRHLVYKVFVSDSM-QKGGSFASYLEEVDCEGE	639	
QY	161	-----NIVMPQFTEAVSPSV	175	
Db	640	DHCEHVCVNTLGSYBCTCKIGYELHSDGKCKEACGGYLDAPSGTISSPSF-----	694	
QY	176	LPSPALPLDLNNAITAFS-----TLEDIIRYLEPERWQLDLEDLYRPTWQLLGKAFVG	230	
Db	695	YPPD-----KNCVWHISAPKGHTITVNFTHMDLE-WRGDECEL-----DFVRVTNVVG	741	
QY	231	RKSRVVDLNLITVEVRLSYCTPENSFVS--IREELKRTDTIFWPGCLL-----VKRCGN	283	
Db	742	NKER-----LQGYCGFWAPSPITSLSNELRIEPRNSDDTLQKTFGSMYDVAVDDECASS	795	
QY	284	CACCLHNCN-----ECQC	296	

Search completed: November 25, 2003, 21:05:29
Job time : 15.7173 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:55:48 ; Search time 8.55655 Seconds
(without alignments)
1896.117 Million cell updates/sec

Title: US-09-852-209A-3

Sequence: 1 MSUFGLLVTSALAQRRGT.....DVALEHHECDVCVRGSGTGG 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	179.5	9.7	928	1 NRPI_XENLA	P28824 xenopus lae
2	176	9.5	707	1 NRPI_XENLA	P98070 xenopus lae
3	173.5	9.3	616	1 SPAN_STRPU	P98068 strongyloce
4	169	9.1	986	1 NRPI_HUMAN	P13497 homo sapien
5	169	9.1	991	1 NRPI_MOUSE	P98063 mus musculu
6	164.5	8.9	931	1 NRPI_HUMAN	O60462 homo sapien
7	163.5	8.8	922	1 NRPI_RAT	Q9GWI9 rattus norv
8	163	8.8	925	1 NRPI_RAT	O35276 rattus norv
9	162.5	8.7	926	1 NRPI_RAT	O35251 rattus norv
10	160.5	8.6	923	1 NRPI_MOUSE	P97333 mus musculu
11	160.5	8.6	931	1 NRPI_MOUSE	O35375 mus musculu
12	159	8.6	1022	1 TLD_BRARE	O57460 brachydanio
13	158.5	8.5	923	1 NRPI_HUMAN	O14786 homo sapien
14	157	8.4	914	1 NRPI_CHICK	P79795 gallus gall
15	154	8.3	449	1 PCOI_HUMAN	Q15113 homo sapien
16	148.5	8.0	1057	1 TLD_DROME	P25723 drosophila
17	147	7.9	354	1 NRPI_HUMAN	O43915 homo sapien
18	143.5	7.7	686	1 NRPI_HUMAN	O00187 homo sapien
19	140	7.5	358	1 NRPI_MOUSE	P97946 mus musculu
20	139.5	7.5	597	1 NRPI_PARLI	P97946 mus musculu
21	138.5	7.5	704	1 NRPI_MOUSE	P98064 mus musculu
22	138	7.4	639	1 NRPI_MOUSE	P98069 strongyloce
23	138	7.4	705	1 NRPI_HUMAN	P00736 homo sapien
24	137.5	7.4	699	1 NRPI_HUMAN	P48740 h complemen
25	132	7.1	419	1 NRPI_MOUSE	P49767 homo sapien
26	128	6.9	468	1 NRPI_MOUSE	Q61398 mus musculu
27	128	6.9	468	1 NRPI_MOUSE	O98628 rattus norv
28	125	6.7	213	1 NRPI_MOUSE	P34007 oryctolagus
29	125	6.7	415	1 NRPI_MOUSE	P97953 mus musculu
30	123.5	6.6	277	1 NRPI_MOUSE	P98066 homo sapien
31	120.5	6.5	245	1 NRPI_MOUSE	P12919 felis silve
32	120.5	6.5	275	1 NRPI_MOUSE	O98859 mus musculu
33	118.5	6.4	276	1 NRPI_MOUSE	P98065 oryctolagus

RESULT 1

ID	NRPI_XENLA	STANDARD;	PRT;	928 AA.
AC	P28824;			
DT	01-DEC-1992 (Rel. 24, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Neuropilin-1 precursor (A5 protein) (A5 antigen).			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8395;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=91337458; PubMed=1908252;			
RA	Takagi S, Hirata T, Agata K, Mochii M, Eguchi G, Fujisawa H;			
RT	"The A5 antigen, a candidate for the neuronal recognition molecule,			
RL	Neuron 7:295-307(1991).			
CC	-I- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE			
CC	CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF			
CC	CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS			
CC	SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS (BY			
CC	SIMILARITY). PRESUMED TO BE INVOLVED IN THE NEURONAL RECOGNITION			
CC	BETWEEN THE OPTIC NERVE FIBERS AND THE VISUAL CENTERS.			
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-I- TISSUE SPECIFICITY: RETINAL GANGLION CELLS AND VISUAL CENTER			
CC	NEURONS.			
CC	-I- SIMILARITY: BELONGS TO THE NEUROFILIN FAMILY.			
CC	-I- SIMILARITY: Contains 2 CUB domains.			
CC	-I- SIMILARITY: Contains 2 F5/8 type C domains.			
CC	-I- SIMILARITY: Contains 1 MAM domain.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; D10467; BAA01260.1; -.			
DR	HSSP; P12259; 1C2T.			
DR	InterPro: IPR000859; CUB domain.			
DR	InterPro: IPR000421; FAS8 C.			
DR	InterPro: IPR000998; MAM domain.			
DR	Pfam; PF00431; CUB; 2.			
DR	Pfam; PF00754; F5 F8 type C; 2.			
DR	Pfam; PF00629; MAM; 1.			
DR	PRINTS; PR00020; MAMDOMAIN.			
DR	SMART; SM00042; CUB; 2.			
DR	SMART; SM00231; FAS8C; 2.			
DR	SMART; SM00137; MAM; 1.			
DR	PROSITE; PS01180; CUB; 2.			

P52585 orf virus (

P01127 homo sapien

P13698 xenopus lae

P42664 xenopus lae

P20033 mus musculu

P28576 rattus norv

P26617 cavia porce

P01128 simian sarc

P49765 homo sapien

P15692 homo sapien

P04085 homo sapien

P52584 orf virus (

ALIGNMENTS

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DR PROSITE; PS01285; FA58C 1; 2.
DR PROSITE; PS01286; FA58C 2; 2.
DR PROSITE; PS00022; FA58C 3; 2.
DR PROSITE; PS00740; MAM 1; 1.
DR PROSITE; PS00606; MAM 2; 1.
KW Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
KW Receptor; Antigen.
FT SIGNAL 1 21
FT CHAIN 22 928
FT DOMAIN 22 860
FT TRANSMEM 861 883
FT DOMAIN 884 928
FT DOMAIN 928 141
FT DOMAIN 141 265
FT DOMAIN 265 424
FT DOMAIN 424 584
FT DOMAIN 584 812
FT DOMAIN 812 104
FT DISULFID 104 173
FT DISULFID 173 228
FT DISULFID 228 265
FT DISULFID 265 424
FT DISULFID 424 584
FT CARBOHYD 584 150
FT CARBOHYD 150 261
FT CARBOHYD 261 300
FT CARBOHYD 300 523
FT CARBOHYD 523 844
FT CARBOHYD 844 928
SQ SEQUENCE 928 AA; 103416 MW; AF6B32380A4C789D CRC64;

Query Match 9.7%; Score 179.5; DB 1; Length 928;
Best Local Similarity 31.6%; Pred. No. 2e-07;
Matches 55; Conservative 29; Mismatches 73; Indels 17; Gaps 7;

QY 50 ITVSTNGSIHSPRPHTYPRNTVLVRLVAEENVWLTDERFGLDEDDICKYDFV 109
DB 31 IKITSPSLTSGAGPHSPYPPQRCWLIQAEHYQVRIMNPNHFDLEDRE--CKYDYV 87

QY 110 EV--EPPSDGILGRWCGSGVPGKQISKQIRIRFVSDYFPPGFCIHYNVMP-- 165
DB 88 EVIDGDNAGQLLKYCKCK-TAPSLVSTGSIPIRFSVDYETPG-AGFSRYEVFKTGP 145

QY 166 ----QFTRA--VSPSVLPSPALPDLINNAITASTLEDLIRYLEPERWQLDLE 213
DB 146 ECSNFTSSNGVIKSPYKPYNALECTYIIFAPKQIEIV--LEFESFELEAD 197

RESULT 2
BNP1_XENLA
ID BNPI_XENLA STANDARD; PRT; 707 AA.
AC P98070;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bone morphogenetic protein 1 precursor (EC 3.4.24.-) (BMP-1).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=81355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo.
RX MEDLINE=94085787; PubMed=8262384;
RA Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;
RT "Cloning and expression of cDNA encoding Xenopus laevis bone
RT morphogenetic protein-1 during early embryonic development.";
RL Gene 134:257-261(1993).
CC -!- FUNCTION: INVOLVED IN PATTERN FORMATION IN GASTRULA AND LATER
CC DIFFERENTIATION OF DEVELOPING ORGANS.
CC -!- DEVELOPMENTAL STAGE: BLASTULA, EARLY GASTRULA AND HATCHED
CC TADPOLES; LITTLE OR NO EXPRESSION IN MORULA AND LATE GASTRULA.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.

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CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 3 CUB domains.
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CC or send an email to license@isb-sib.ch).
CC EMBL; LI2249; AAL16313.1; -.
CC PIR; JC2218; JC2218.
CC HSSP; P00736; LAPQ.
CC MEROPS; M12.005; -.
CC InterPro; IPR001506; Astacin.
CC InterPro; IPR000152; Asx_hydroxyl.
CC InterPro; IPR000859; CUB_domain.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR006026; NZn_Mtpeptidse.
CC InterPro; IPR006025; Zn_Mtpeptidse.
CC Pfam; PF01400; Astacin; 1.
CC Pfam; PF00431; CUB; 3.
CC Pfam; PF00008; EGF; 1.
CC PRINTS; PRO00480; ASTACIN.
CC SMART; SM00042; CUB; 3.
CC SMART; SM00179; EGF_CA; 1.
CC SMART; SM00235; ZNMG; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC PROSITE; PS01180; CUB; 3.
CC PROSITE; PS001010; ASX_HYDROXYL; 1.
CC PROSITE; PS00022; EGF_1; FALSE_NEG.
CC PROSITE; PS01186; EGF_2; 1.
CC PROSITE; PS01187; EGF_CA; 1.
KW Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase; Protease;
KW Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
KW Glycoprotein.
FT SIGNAL 1 ? POTENTIAL.
FT PROPEP 2 83 POTENTIAL.
FT CHAIN 84 707 BONE MORPHOGENETIC PROTEIN 1.
FT DOMAIN 84 284 METALLOPROTEASE.
FT DOMAIN 285 397 CUB 1.
FT DOMAIN 398 509 CUB 2.
FT DOMAIN 510 551 EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 554 666 CUB 3.
FT METAL 176 177 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 177 177 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 180 180 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 186 186 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 146 149 BY SIMILARITY.
FT DISULFID 514 526 BY SIMILARITY.
FT DISULFID 522 535 BY SIMILARITY.
FT DISULFID 537 550 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 326 326 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 562 562 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 707 AA; 80673 MW; 1B6980D716DC98D CRC64;

Query Match 9.5%; Score 176; DB 1; Length 707;
Best Local Similarity 43.3%; Pred. No. 2.9e-07;
Matches 45; Conservative 15; Mismatches 36; Indels 8; Gaps 5;

QY 55 NGSIHSPRPHTYPRNTVLVRLVAEENVWLTDERFGLDEDDICKYDFVEVEE- 113
DB 562 NGSINSGWPKYPPNKNCIQWLVAPTQ-YRISLQFDQ--FETEGNDCKYDFVEVRSG 617

QY 114 -PSDGTILGRWCGSGVPGKQISKQIRIRFVSDYFPPGFCIHYNVMP-- 156
DB 618 L7SDSKLHGKFGGS-ELPAVITVSNYNNMIRIFPKSDNTV-SKKGF 659

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RESULT 3
 SPAN STRPU STANDARD; PRT; 616 AA.
 ID SPAN STRPU STANDARD; PRT; 616 AA.
 AC P9068;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE SPAN protein precursor (EC 3.4.24.-).
 GN SPAN.
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinozoa; Echinozoa; Echinodermata; Eleutherozoa; Echinozoa; Strongylocentrotidae;
 OC Strongylocentrotus.
 OX NCBI_TaxID=7668;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=923115921; PubMed=1618141;
 RA Reynolds S.D., Angerer L.M., Palle J., Nasir A., Angerer R.C.;
 RT "Early mRNAs, spatially restricted along the animal-vegetal axis of
 sea urchin embryos, include one encoding a protein related to tollid
 and BMP-1."
 RL Development 114:769-786(1992).
 CC -!- TISSUE SPECIFICITY: ASYMMETRICALLY ALONG THE ANIMAL-VEGETAL AXIS
 OF THE BLASTULA.
 CC -!- DEVELOPMENTAL STAGE: VERY EARLY BLASTULA (BETWEEN 16-CELL STAGE
 AND HATCHING).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 CC -!- SIMILARITY: Contains 2 CUB domains.
 CC
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 CC
 CC EMBL; M84144; AAA30072.1; -;
 DR HSP; P28825; 11AF.
 DR MEROPS; M12.013; -;
 DR InterPro; IPR001506; Astacin.
 DR InterPro; IPR000859; CUB domain.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR006026; Zn MTpeptidse.
 DR InterPro; IPR006025; Zn MTpeptidse.
 DR Pfam; PF01400; Astacin; 1.
 DR Pfam; PF00431; CUB; 2.
 DR PRINTS; PR00480; ASTACIN.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00235; ZnMC; 1.
 DR PROSITE; PS00142; ZINC PROTEASE; 1.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS00022; EGF; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR Developmental protein; Repeat; Hydrolase; Protease; Zinc; Embryo;
 KW Metalloprotease; EGF-like domain; Signal.
 FT SIGNAL 1 16
 FT PROPEP 17 93
 FT CHAIN 94 616
 FT DOMAIN 89 93
 FT DOMAIN 94 295
 FT DOMAIN 295 329
 FT DOMAIN 340 450
 FT DOMAIN 451 502
 FT DOMAIN 503 614
 FT METAL 190 190
 FT ACT SITE 191 191
 FT METAL 194 194
 FT METAL 194 200
 FT METAL 200 200

FT DISULFID 299 315 BY SIMILARITY.
 FT DISULFID 305 317 BY SIMILARITY.
 FT DISULFID 319 328 BY SIMILARITY.
 SQ SEQUENCE 616 AA; 67902 MW; 397CD923PFB9EB98 CRC64;
 Query Match 9.3%; Score 173.5; DB 1; Length 616;
 Best Local Similarity 27.0%; Pred. No. 3.9e-07;
 Matches 70; Conservative 33; Mismatches 93; Indels 63; Gaps 14;
 QY 56 GSIHSPREPHTYPRNTVLVRLVAEENVMVLTQTFDFRFGLEDPEDDICKYDFVEVEEPS 115
 Db 349 GRITSPNPSYVEDNTACVYIEGPGYST-IELTF--LMEIETETLCRYDAVEVRKDD 404
 QY 116 DGTILGRMGSGTVPKQISKGNQIRIRFVSDEYFPPS--EPGCIHYNIVMQPTEAVSP 173
 Db 405 INSIGKFCGN-TLPVQVSSNQMVSTSD---PSITRKGKATVVIIL-QTTTFVST 459
 QY 174 SVL---PPSALPLDLLNNAITAFSTLEDLIRYLEPERMQLEDLYRPTMOLGKAFVFG 230
 Db 460 TLTQTPPSTTTTLQTNFSTTLQI-----TNPSTTLQTTD--TPVIGSCGTFV-G 509
 QY 231 RKSRRVDNLLTEVRLVYSCTRPFSVIR-----BELKRTDIF-----W 271
 Db 510 VEGRVASPNY-----PNQYDNLQCDYVVDGRRVELLPEDFGLEDTETCRW 558
 QY 272 PGCLL-----VKRQG 281
 Db 559 DSLMINLNGIKVGMKMG 577
 RESULT 4
 BMP1 HUMAN
 ID BMP1 HUMAN STANDARD; PRT; 986 AA.
 AC P13497; Q13292; Q13872; Q14874; Q99421; Q99422; Q99423; Q9UL38;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
 DE (Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mtld).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM BMP1-3).
 RC TISSUE=Skin;
 RX MEDLINE=96209868; PubMed=8643539;
 RA Li S.W., Sieron A.L., Fertala A., Hojima Y., Arnold W.V.,
 RA Prockop D.J.;
 RT "The C-proteinase that processes procollagens to fibrillar collagens
 is identical to the protein previously identified as bone morphogenic
 protein-1."
 RT Proc. Natl. Acad. Sci. U.S.A. 93:5127-5130(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM BMP1-1).
 RX MEDLINE=89072730; PubMed=3201241;
 RA Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitters M.J.,
 RA Kriz R.W., Hewick R.M., Wang E.A.;
 RT "Novel regulators of bone formation: molecular clones and
 activities."
 RT Science 242:1528-1534(1988).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS BMP1-4; BMP1-5 AND BMP1-6).
 RC TISSUE=Placenta;
 RX MEDLINE=98160316; PubMed=9500680;
 RA Janitz M., Heiser V., Boettcher U., Landt O., Lauter R.;
 RT "Three alternatively spliced variants of the gene coding for the human
 bone morphogenetic protein-1."
 RN [4]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS BMP1-3 AND BMP1-7).
 RC TISSUE=Placenta;

RX MEDLINE=95096114; PubMed=7798260;
RA Takahara K., Lyons G.E., Greenspan D.S.;
RT "Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld)
RT are encoded by alternatively spliced transcripts which are
RT differentially expressed in some tissues";
RL J. Biol. Chem. 269:32572-32578(1994).
RN (5)
RP DISULFIDE BOND IN METALLOPROTEASE DOMAIN.
RX MEDLINE=21336528; PubMed=11283002;
RA Garrigue-Antar L., Barker C., Kadler K.E.;
RT "Identification of amino acid residues in bone morphogenetic
RT protein-1 important for procollagen C-proteinase activity";
RL J. Biol. Chem. 276:26237-26242(2001).
CC -!- FUNCTION: CLEAVES THE C-TERMINAL PROPEPTIDES OF PROCOLLAGEN I, II
CC AND II. INDUCES CARTILAGE AND BONE FORMATION.
CC -!- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at
CC Ala--Asp in type I and II procollagens and at Arg--Asp in type
CC III.
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-
CC -!- ENDOPEPTIDASE ENHANCER PROTEIN.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=7;
CC Name=BMP1-3;
CC IsoId=p13497-1; Sequence=VSP_005461, VSP_005462;
CC IsoId=p13497-2; Sequence=VSP_005461, VSP_005462;
CC Name=BMP1-1;
CC IsoId=p13497-7; Sequence=Not described;
CC Name=BMP1-4;
CC IsoId=p13497-3; Sequence=VSP_005463, VSP_005464;
CC Name=BMP1-5;
CC IsoId=p13497-4; Sequence=VSP_005465, VSP_005466;
CC Name=BMP1-6;
CC IsoId=p13497-5; Sequence=VSP_005467, VSP_005468;
CC Name=BMP1-7;
CC IsoId=p13497-6; Sequence=VSP_005469, VSP_005470;
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 5 CUB domains.
CC -----
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CC -----
DR EMBL; U50330; AAA93462.1; -;
DR EMBL; M22488; AAA51833.1; -;
DR EMBL; Y08723; CAA69973.1; -;
DR EMBL; Y08724; CAA69974.1; -;
DR EMBL; Y08725; CAA69975.1; -;
DR EMBL; L35278; AAC41703.1; -;
DR EMBL; L35279; AAC41710.1; -;
DR PIR; A37278; B58788.
DR HSP; P00736; IAFQ.
DR MEROPS; M12.005; -;
DR Genew; HGNC:1067; BMP1.
DR MIM; 112264; -;
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:000237; F:metallopeptidase activity; NAS.
DR GO; GO:0001502; F:cartilage condensation; TAS.
DR GO; GO:0007275; F:development; TAS.
DR InterPro; IPR001506; Astacin.
DR InterPro; IPR00152; Asx hydroxyl.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006026; Nzn_Mtpeptdse.
DR InterPro; IPR006025; Zn_Mtpeptdse.
DR Pfam; PF01400; Astacin; 1.
DR Pfam; PF00431; CUB; 5.
DR Pfam; PF00008; EGF; 2.
DR PRINTS; PR00480; ASTACIN.
DR SMART; SM00042; CUB; 5.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00235; ZmC; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS01180; CUB; 5.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_Ca; 2.
KW Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase;
KW Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
KW Glycoprotein; Zymogen; Alternative splicing.
FT SIGNAL 1 22
FT POTENTIAL.
FT PROPEP 23 120
FT CHAIN 121 986
FT BONE MORPHOGENETIC PROTEIN 1.
FT DOMAIN 121 321
FT METALLOPROTEASE.
FT DOMAIN 322 434
FT CUB 1.
FT DOMAIN 435 546
FT CUB 2.
FT DOMAIN 547 588
FT CUB 3.
FT DOMAIN 591 703
FT EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT CUB 4.
FT DOMAIN 747 859
FT CUB 5.
FT METAL 213 213
FT ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 214 214
FT BY SIMILARITY.
FT METAL 217 217
FT ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 223 223
FT ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 183 186
FT BY SIMILARITY.
FT DISULFID 322 348
FT BY SIMILARITY.
FT DISULFID 375 397
FT BY SIMILARITY.
FT DISULFID 435 461
FT BY SIMILARITY.
FT DISULFID 488 510
FT BY SIMILARITY.
FT DISULFID 551 563
FT BY SIMILARITY.
FT DISULFID 559 572
FT BY SIMILARITY.
FT DISULFID 574 587
FT BY SIMILARITY.
FT DISULFID 591 617
FT BY SIMILARITY.
FT DISULFID 644 666
FT BY SIMILARITY.
FT DISULFID 707 718
FT BY SIMILARITY.
FT DISULFID 714 727
FT BY SIMILARITY.
FT DISULFID 729 742
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 91 91
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 363 363
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 599 599
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 703 730
DR RGRPHOLKFRVQRNRTPO (in isoform BMP1-1).
FT /FTID=VSP_005461.
DR Missing (in isoform BMP1-1).
FT /FTID=VSP_005462.
DR OEYVFLKMEPQVESIGETDYDFDSIMHVARNTFSRGIFLDT
FT IYKPEYGVKPIQOR > VLHSLLLSCGSRNGASFP
FT CSLESTHQLCWTGLFRLPSPFPFLAAPTFLRGV
FT (in isoform BMP1-4).
FT /FTID=VSP_005463.
DR Missing (in isoform BMP1-4).
FT /FTID=VSP_005464.
DR AACGGFLKNGSITSPGMPKVPNNKNCIMOLV -> GCY
FT DLQVKGFLNDRHCFRLSTHGFEMGLTALRG (in
FT isoform BMP1-5).
FT /FTID=VSP_005465.
DR Missing (in isoform BMP1-5).
FT /FTID=VSP_005466.
DR DKDECKNGGCGQD -> GGELFGLGHPPRRP (in
FT isoform BMP1-6).
FT /FTID=VSP_005467.
DR Missing (in isoform BMP1-6).
FT /FTID=VSP_005468.
DR DKDECKNGGCGQDVFNTFGSYECQCR -> EKRPALQPP

Db 659 GLTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKGGFKAHF 705

RESULT 6

NRP2_HUMAN STANDARD; PRT; 931 AA.
 ID NR2P2_HUMAN STANDARD; PRT; 931 AA.
 AC O60462; O14820; O14821;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2)
 GN NR2P2 OR VEGF165R2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS A0 AND A17).
 RX MEDLINE=97470888; PubMed=9331348;
 RA Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
 RT "Neuropilin-2, a novel member of the neuropilin family, is a high affinity receptor for the semaphorins Sema E and Sema IV but not Sema III.";
 RL Neuron 19:547-559(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM A22).
 RC TISSUE=Brain;
 RX MEDLINE=9818099; PubMed=9529250;
 RA Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.;
 RT "Neuropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor.";
 RL Cell 92:735-745(1998).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=20309748; PubMed=10748121;
 RA Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
 RT "Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid form of vascular endothelial growth factor (VEGF) and of placenta growth factor-2, but only neuropilin-2 functions as a receptor for the 145-amino acid form of VEGF.";
 RL J. Biol. Chem. 275:18040-18045(2000).
 CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165 AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
 CC -!- SUBUNIT: NEUROFILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH NEUROFILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN 3C RECEPTOR.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=A22;
 CC IsoId=O60462-1; Sequence=Displayed;
 CC Name=A0;
 CC IsoId=O60462-2; Sequence=VSP_004342;
 CC Name=A17;
 CC IsoId=O60462-3; Sequence=VSP_004341;
 CC -!- SIMILARITY: BELONGS TO THE NEUROFILIN FAMILY.
 CC -!- SIMILARITY: Contains 2 CUB domains.
 CC -!- SIMILARITY: Contains 2 FS/8 type C domains.
 CC -!- SIMILARITY: Contains 1 MAM domain.
 CC -----
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 CC -----
 CC EMBL; AF022859; AAC51788.1; -;
 CC EMBL; AF022860; AAC51789.1; -;
 CC EMBL; AF016098; AAC12922.1; -;
 CC HSPF; F12259; LC21.
 CC Genew; HGNC:8005; NRP2.

DR MIM; 602070; -. C:membrane fraction; TAS.
 DR GO; GO:0005624; -. C:membrane fraction; TAS.
 DR GO; GO:0004872; P:vascular activity; TAS.
 DR GO; GO:0005021; P:vascular endothelial growth factor receptor. . .; TAS.
 DR GO; GO:0007411; P:axon guidance; TAS.
 DR InterPro; IPR000859; CUB domain.
 DR InterPro; IPR000421; FAS8_C.
 DR InterPro; IPR000998; MAM_domain.
 DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00754; F5 F8 type C; 2.
 DR Pfam; PF00629; MAM; 1.
 DR PRINTS; PR00020; MAMDOMAIN.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00231; FAS8C; 2.
 DR SMART; SM00137; MAM; 1.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS01285; FAS8C_1; 2.
 DR PROSITE; PS01286; FAS8C_2; 2.
 DR PROSITE; PS00022; FAS8C_3; 2.
 DR PROSITE; PS50060; MAM_2; 1.
 DR Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor;
 KW Alternative splicing.
 FT SIGNAL 1 20 OR 22 (POTENTIAL).
 FT CHAIN 21 931 NEUROFILIN-2.
 FT DOMAIN 21 864 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 865 889 POTENTIAL.
 FT DOMAIN 890 931 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 28 142 CUB 1.
 FT DOMAIN 149 267 CUB 2.
 FT DOMAIN 277 427 F5/8 TYPE C 1.
 FT DOMAIN 434 592 F5/8 TYPE C 2.
 FT DOMAIN 642 802 MAM.
 FT DOMAIN 671 674 POLY-SER.
 FT DISULFID 28 55 BY SIMILARITY.
 FT DISULFID 83 105 BY SIMILARITY.
 FT DISULFID 149 175 BY SIMILARITY.
 FT DISULFID 208 230 BY SIMILARITY.
 FT DISULFID 277 427 BY SIMILARITY.
 FT DISULFID 434 592 BY SIMILARITY.
 FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 809 813 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 830 813 Missing (in isoform A17).
 FT VARSPLIC 830 830 Missing (in isoform A0).
 FT CONFLICT 602 602 E -> K (IN REF. 1).
 FT SEQUENCE 931 AA; 104830 MW; 270CBAB69A0A797C CRC64;
 Query Match 8.9%; Score 164.5; DB 1; Length 931;
 Best Local Similarity 29.9%; Pred. No. 3.9e-06;
 Matches 49; Conservative 20; Mismatches 70; Indels 25; Gaps 5;
 QY 1 MSLGLLLVTSALAGQRRGTQAEENLSKQFSSNKQNGVQDPQHERIITVSTNGSIHS 60
 Db 1 MDMPFLTWVFLAL-----YFSHQVGRGQDPPPCGRLNSKDAGYITS 42
 QY 61 PRFHTYPRNTVLYVRLVAVENVWIQLTFDEREGLEDPEDDICKYDFVEVE--EPSDGT 118
 Db 43 PGYQDYPSHQNCWVIVAPNPQKIVLNFNPFIEKHD---CKYDFIEIRDGDSAD 99
 QY 119 ILGRCWCSGTVPQKISGKQIRIRFVSDYFFSEPGFCIHNYI 162
 Db 100 LLGKHCNG-IAPPTIISSGMLYIKFTSD-YARQAGGFSLEYI 141
 RESULT 7
 NRP1_RAT
 ID NRP1_RAT
 AC Q9QWJ9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropilin-1 precursor (Vascular endothelial cell growth factor 165
DE receptor)
GN NP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97433085; PubMed=9288754;
RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
RA Ginty D.D.;
RL Cell 90:753-762(1997).
CC -1- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CC CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF
CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS
CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT
CC BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165
CC ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN
CC INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.
CC IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: FOUND IN THE EMBRYONIC NERVOUS SYSTEM.
CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
CC -1- SIMILARITY: Contains 1 MAM domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF016296; AAC53337.1; -.
DR HSSP; P12259; 1CZT.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000421; FA58_C.
DR InterPro; IPR000998; MAM domain.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00754; F5_F8_type_C; 2.
DR Pfam; PF00629; MAM; 1.
DR PRINTS; PR00020; MAMDOMAIN.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FA58C; 2.
DR SMART; SM00137; MAM; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FA58C_1; 2.
DR PROSITE; PS01286; FA58C_2; 2.
DR PROSITE; PS00022; FA58C_3; 2.
DR PROSITE; PS00740; MAM; 1; 1.
DR PROSITE; PS00600; MAM; 2; 1.
DR PROSITE; PS00600; MAM; 2; 1.
KW Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
KW Receptor.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 922 NEUROPILIN-1.
FT DOMAIN 22 855 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 856 880 POTENTIAL.
FT DOMAIN 881 922 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 27 141 CUB 1.
FT DOMAIN 147 265 CUB 2.
FT DOMAIN 275 424 F5/8 TYPE C 1.
FT DOMAIN 431 583 F5/8 TYPE C 2.
FT DOMAIN 645 811 MAM.
FT DOMAIN 27 54 PROBABLE.
FT DISULFID 82 104 PROBABLE.
FT DISULFID 147 173 PROBABLE.
FT DISULFID 206 228 PROBABLE.

FT DISULFID 275 424 BY SIMILARITY.
FT DISULFID 431 583 BY SIMILARITY.
FT CARBOHYD 150 150 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 522 522 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 841 841 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 922 AA, 103082 MW, CC6F82AD098B0F2E CRC64;
Query Match 8.8%; Score 163.5; DB 1; Length 922;
Best Local Similarity 36.5%; Pred. No. 4.7e-06;
Matches 42; Conservative 16; Mismatches 50; Indels 7; Gaps 4;
QY 50 ITVTGNSIHSPPPHYPRNTLVLRVLAEEVNVQLTFDERFGLDEDDICKYDFV 109
DB 31 IKIENPGVLTSPGYPHSHYSEKCEWLIQAEPPQRTIMINPHFDLED RD---CKDYV 87
QY 110 EV--EFPSDGTILGRWCSTGTPQKQISKNQIRIRFVSDEYFSPSPGCHYNI 162
DB 88 EVIDGENEGRLMGKFCGK-IAPSPVWSSGPFIFKEVSD-YETHGAGFSIRYEI 140
RESULT 8
NRP2 RAT
ID NRP2 RAT STANDARD; PRT; 925 AA.
AC O35276;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165
DE receptor 2).
GN NRP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97433085; PubMed=9288754;
RA Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
RA Ginty D.D.;
RL Cell 90:753-762(1997).
CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
CC AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: FOUND IN CERTAIN NEURONAL POPULATIONS OF THE
CC CNS AND IN OTHER NONNEURONAL TISSUES INCLUDING MESENCHYMAL TISSUE
CC LINING IN THE RIBS.
CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
CC -1- SIMILARITY: Contains 1 MAM domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF016297; AAC53338.1; -.
DR HSSP; P12259; 1CZT.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000421; FA58_C.
DR InterPro; IPR000998; MAM domain.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00754; F5_F8_type_C; 2.
DR Pfam; PF00629; MAM; 1.
DR PRINTS; PR00020; MAMDOMAIN.
DR SMART; SM00042; CUB; 2.

NRPI_MOUSE
ID NRPI_MOUSE STANDARD; PRT; 923 AA.
AC P97333;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT NRPI_MOUSE precursor (A5 protein).
DE NRPI_MOUSE precursor (A5 protein).
GN NRPI_MOUSE precursor (A5 protein).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C; TISSUE=Embryonic brain;
RA MEDLINE=96353149; PubMed=8748368;
RA Kawakami A., Katsukawa T., Takagi S., Fujisawa H.;
RT "Developmentally regulated expression of a cell surface protein,
neuropilin, in the mouse nervous system.";
RL J. Neurobiol. 29:1-17(1996).
CC -1- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS. IN THE FORMATION OF
CC SYSTEMS. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT
CC BINDS TO SEMAPHORIN 3A, THE PLGF-2 ISOFORM OF VEGF, THE VEGF-165
CC ISOFORM OF VEGF AND VEGF-B. COEXPRESSION WITH KDR RESULTS IN
CC INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.
CC IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -1- TISSUE SPECIFICITY: NERVOUS SYSTEM.
CC -1- SIMILARITY: BELONGS TO THE NEUROFILIN FAMILY.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
CC -1- SIMILARITY: Contains 1 FAM domain.
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D50086; BAA08789.1; -;
CC HSP; P12259; ICZT.
CC MGD; MGI:106206; Nrp.
CC InterPro; IPR000859; CUB domain.
CC InterPro; IPR000421; FA58_C.
CC InterPro; IPR000998; FAM domain.
CC Pfam; PF00431; CUB; 2.
CC Pfam; PF00754; F5 F8 type_C; 2.
CC Pfam; PF00629; FAM; 1.
CC PRINTS; PR00020; MAMDOMAIN.
CC SMART; SM00042; CUB; 2.
CC SMART; SM00231; FA58C; 2.
CC SMART; SM00137; FAM; 1.
CC PROSITE; PS01180; CUB; 2.
CC PROSITE; PS01285; FA58C_1; 2.
CC PROSITE; PS01286; FA58C_2; 2.
CC PROSITE; PS01286; FA58C_3; 2.
CC PROSITE; PS00740; MAM_1; 1.
CC PROSITE; PS00600; MAM_2; 1.
KW Angiogenesis; Transmembrane; Glycoprotein; Neuron; Signal; Repeat;
Receptor.
FT SIGNAL 1 21
FT CHAIN 22 923
FT DOMAIN 22 856
FT TRANSMEM 857 879
FT DOMAIN 880 923
FT DOMAIN 923 923
FT DOMAIN 27 141
FT DOMAIN 147 265
FT DOMAIN 275 424
FT DOMAIN 431 583

FT DOMAIN 645 811
FT DISULFID 27 54
FT DISULFID 82 104
FT DISULFID 147 173
FT DISULFID 206 228
FT DISULFID 275 424
FT DISULFID 431 583
FT CARBOHYD 150 150
FT CARBOHYD 261 261
FT CARBOHYD 300 300
FT CARBOHYD 522 522
FT CARBOHYD 842 842
SQ SEQUENCE 923 AA; 103020 MW; 0644B8A170796808 CRC64;
Query Match 8.6%; Score 160.5; DB 1; Length 923;
Best Local Similarity 36.5%; Pred. No. 8.5e-06;
Matches 42; Conservative 16; Mismatches 50; Indels 7; Gaps 4;
QY 50 ITVTNGSIHSPRPHPTNTLVRLVAVENWVMIQLTDFRFGLEDPEDDICKYDFV 109
DB 31 IKIENPGVLTSPGYSHYHPEKCEWLIOAPEYQRIINFNPHFDLEDRD---CKYDV 87
QY 110 EV--EPPSGDTILGRWCSGTVPQKISKGNQIRFVSDVEYFPPEPGFCHWNI 162
DB 88 EVIDGENEGRLMKFCGK-IAPSPVWSSGPFLLFKFVSD-YETHGAGFSIRYEI 140
RESULT 11
NRPI_MOUSE STANDARD; PRT; 931 AA.
AC Q35375; Q35373; Q35374; Q35376; Q35377; Q35378;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropilin-2 precursor (Vascular endothelial cell growth factor 165
DE receptor 2).
GN NRPI_MOUSE
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A0; A17; A22; A5; B0 AND B5).
RC STRAIN=BALE/C;
RX MEDLINE=97470888; PubMed=9331348;
RA Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
RT "Neuropilin-2, a novel member of the neuropilin family, is a high
RT affinity receptor for the semaphorins Sema E and Sema IV but not Sema
RT III.";
RL Neuron 19:547-559(1997).
CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
CC AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF VEGF.
CC -1- SUBUNIT: NEUROFILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH
CC NEUROFILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN E RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-alternative splicing; Named isoforms=6;
CC Name=A22;
CC IsoId=Q35375-1; Sequence=Displayed;
CC Name=A0;
CC IsoId=Q35375-2; Sequence=VSP_004344;
CC Name=A5;
CC IsoId=Q35375-3; Sequence=VSP_004345;
CC Name=A17;
CC IsoId=Q35375-4; Sequence=VSP_004343;
CC Name=B0;
CC IsoId=Q35375-5; Sequence=VSP_004346;
CC Name=B5;
CC IsoId=Q35375-6; Sequence=VSP_004347;
CC -1- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING CNS, PNS AND IN SOME
CC NONNEURAL TISSUES INCLUDING LIMB BUDS, DEVELOPING BONES, MUSCLES,
CC INTESTINAL EPITHELIUM, KIDNEY, LUNG AND SUBMANDIBULAR GLAND.
CC -1- DEVELOPMENTAL STAGE: THE EXPRESSION PATTERN IS VERY DYNAMIC AND IS

semaphorin family. Its expression has an aversive effect on blood vessel number and integrity.

-!- SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is secreted.

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=1; Synonyms=Membrane-bound;

IsoId=O14786-1; Sequence=Displayed;

Name=2; Synonyms=Soluble, SNRP1;

IsoId=O14786-2; Sequence=VSP_004339, VSP_004340;

-!- TISSUE SPECIFICITY: The expression of isoforms 1 and 2 does not seem to overlap. Isoform 1 is expressed by the blood vessels of different tissues. In the developing embryo it is found

predominantly in the nervous system. In adult tissues, it is highly expressed in heart and placenta; moderately in lung, liver, skeletal muscle, kidney and pancreas; and low in adult brain. Isoform 2 is found in liver hepatocytes, kidney distal and proximal tubules.

-!- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.

-!- SIMILARITY: Contains 2 CUB domains.

-!- SIMILARITY: Contains 2 F5/8 type C domains.

-!- SIMILARITY: Contains 1 MAM domain.

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EMBL; AF018956; AAC51759.1; -

EMBL; AF016050; AAC12921.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

EMBL; AF145712; AAF44344.1; -

FT DISULFID 147 173 PROBABLE.
FT DISULFID 206 228 PROBABLE.
FT DISULFID 275 424 BY SIMILARITY.
FT DISULFID 431 583 BY SIMILARITY.
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 842 842 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 642 644 EFP -> GIK (in isoform 2).
FT VARSPLIC 645 923 Missing (in isoform 2).
FT VARSPLIC 645 923 Missing (in isoform 2).
FT CONFLICT 26 26 K -> E (IN REF. 1).
FT CONFLICT 749 749 D -> H (IN REF. 2).
FT CONFLICT 855 855 E -> D (IN REF. 2).
SQ SEQUENCE 923 AA; 103120 MW; ADEADCA4849ESD57 CRC64;

Query Match 8.5%; Score 158.5; DB 1; Length 923;

Best Local Similarity 35.7%; Pred. No. 1.3e-05;

Matches 41; Conservative 18; Mismatches 49; Indels 7; Gaps 4;

QY 50 ITVSTNGSIHSPRPHTYPRNTVLVRLVAVERNVTQLTDERFGLDEDDICKYDFV 109

Db 31 IKIESPGVLTSPGYHSPSEKWLQAPDPYQIRIMINFNHFDLEDRD---CKYDYV 87

QY 110 EV--EESDGTILGRMGSGTVPGKQISKGNQIRFVSDEYFSPSEPGCIHNYI 162

Db 88 EVFDGNEHFRGKFCGK-IAPPVVSQPFIFKFEVSD-YETHGAGFSIRYEI 140

RESULT 14

NRPI_CHICK

ID NRPI_CHICK STANDARD; PRT; 914 AA.

AC P79795;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neuropilin-1 precursor (A5 protein).

GN NRPI OR NRP.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=White leghorn; TISSUE=Embryonic brain;

RX MEDLINE=95324761; PubMed=7601310;

RA Takagi S., Kasuya Y., Shimizu M., Matsuura T., Tsuboi M., Kawakami A.,

RA Fujisawa H.;

RT "Expression of a cell adhesion molecule, neuropilin, in the

RL Dev. Biol. 170:207-222(1995)."

CC -!- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE

CC CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF

CC CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS

CC SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS (BY

CC SIMILARITY). SEEMS TO HAVE CALCIUM-INDEPENDENT CELL ADHESION

CC PROPERTIES.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: DEVELOPING NERVOUS SYSTEM; OPTIC TECTUM

CC (LAYERS D AND E OF SGFS), AMACRINE CELLS OF RETINA, NEURITES OF

CC DORSAL ROOT GANGLIA. ALSO EXPRESSED IN NONNEURONAL CELLS, E.G.

CC BLOOD VESSEL IN THE ENTIRE EMBRYO.

CC -!- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.

CC -!- SIMILARITY: Contains 2 CUB domains.

CC -!- SIMILARITY: Contains 2 F5/8 type C domains.

CC -!- SIMILARITY: Contains 1 MAM domain.

CC -!- SIMILARITY: Contains 1 MAM domain.

CC -!- SIMILARITY: Contains 1 MAM domain.

CC -!- SIMILARITY: Contains 1 MAM domain.

CC -!- SIMILARITY: Contains 1 MAM domain.

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[illegible]

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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:58:59 ; Search time 30.4613 Seconds
(without alignments)
2922.663 Million cell updates/sec

Title: US-09-852-209A-3
Perfect score: 1858
Sequence: 1 MSLFGLLVTSALAGRRGT.....DVALEHHBECDCVCRGSGG 345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1858	100.0	345	Q9NRA1	Q9nra1 homo sapien
2	1851	99.6	345	Q9UL22	Q9ul22 homo sapien
3	1664	89.6	345	Q9QV71	Q9qv71 mus musculus
4	1662	89.5	345	Q8C119	Q8c119 mus musculus
5	1646	88.6	345	Q9EQX6	Q9eqx6 rattus norv
6	1635	88.0	345	Q9JHV8	Q9jvh8 mus musculus
7	1614	86.9	345	Q9I946	Q9i946 gallus gall
8	1260	67.8	258	Q8K429	Q8k429 rattus norv
9	741.5	39.9	370	Q9GZP0	Q9gzp0 homo sapien
10	740.5	39.9	364	Q9BWV5	Q9bwv5 homo sapien
11	737.5	39.7	370	Q925I7	Q925i7 mus musculus
12	736	39.6	370	Q9EQT1	Q9egt1 rattus norv
13	435.5	23.4	261	Q8K2L3	Q8k2l3 mus musculus
14	190.5	10.3	923	Q8QFX6	Q8qfx6 brachydanio
15	190.5	10.3	923	Q8AXP1	Q8axp1 brachydanio
16	183	9.8	3623	Q60494	Q60494 homo sapien

17	182	9.8	691	13	O57658	O57658 gallus gall
18	180	9.7	34	11	Q99JH4	Q99jm4 mus musculus
19	176	9.5	977	13	Q91325	Q91925 xenopus lae
20	176	9.5	3623	11	O70244	O70244 rattus norv
21	172	9.3	1012	11	Q9WVM6	Q9wvm6 mus musculus
22	171	9.2	735	13	O57381	O57381 xenopus lae
23	171	9.2	926	4	Q9UQ00	Q9uq00 homo sapien
24	171	9.2	1015	4	Q9Y6L7	Q9y6l7 homo sapien
25	169	9.1	241	11	Q9Z135	Q9z135 rattus norv
26	165.5	8.9	145	11	Q8BP20	Q8bp20 mus musculus
27	165.5	8.9	926	11	Q8QZY7	Q8qzy7 mus musculus
28	164.5	8.9	555	4	Q9H2E2	Q9h2e2 homo sapien
29	164.5	8.9	901	4	Q9H2E4	Q9h2e4 homo sapien
30	164.5	8.9	901	4	Q9H2D5	Q9h2d5 homo sapien
31	164.5	8.9	906	4	Q9H2D4	Q9h2d4 homo sapien
32	163.5	8.8	906	4	Q9H2E3	Q9h2e3 homo sapien
33	163.5	8.8	921	11	Q9QX38	Q9qx38 rattus norv
34	163.5	8.8	3620	6	Q9TU53	Q9tu53 canis fami
35	161.5	8.7	1007	13	O8J128	O8j128 xenopus lae
36	158.5	8.5	609	4	Q96190	Q96190 homo sapien
37	158.5	8.5	644	4	Q961H5	Q961h5 homo sapien
38	158.5	8.5	704	4	Q9H2E1	Q9h2e1 homo sapien
39	157.5	8.5	919	13	Q8UVR0	Q8uvr0 gallus gall
40	157.5	8.5	936	13	Q8UVQ9	Q8uvq9 gallus gall
41	157	8.4	1008	13	Q9DER7	Q9der7 gallus gall
42	153	8.2	415	4	Q9UKZ9	Q9ukz9 homo sapien
43	153	8.2	1019	13	O57382	O57382 xenopus lae
44	151.5	8.2	326	11	Q91ZE4	Q91ze4 rattus norv
45	151	8.1	276	4	Q9BRH3	Q9brh3 homo sapien

ALIGNMENTS

RESULT 1

Q9NRA1 ID Q9NRA1 PRELIMINARY; PRT; 345 AA.

AC Q9NRA1; AT 01-OCT-2000 (TREMREL. 15, Created)
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)
DT 01-MAR-2003 (TREMREL. 23, Last annotation update)
DE Platelet-derived growth factor C.

OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.

RC TISSUE=Lung;

RX MEDLINE=20268201; PubMed=10806482;

RA Li X., Ponten A., Aase K., Karlsson L., Abramson A., Utela M.,

RA Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,

RA Betsholtz C., Heldin C.-H., Alitalo K., Ostman A., Eriksson U.;

"PDGF-C is a new protease-activated ligand for the PDGF alpha-

RT receptor.";

RL Nat. Cell Biol. 2:302-309(2000).

CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.

DR EMBL; AF244813; AAF80597.1; -

DR InterPro; HGNC:8801; PDGFC.

DR InterPro; IPR000859; CUB domain.

DR Pfam; PF00431; CUB; 1.

DR SMART; SM00042; CUB; 1.

DR SMART; SM00141; PDGF; 1.

DR PROSITE; PS01180; CUB; 1.

DR PROSITE; PS02078; PDGF 2; 1.

SQ SEQUENCE 345 AA; 35043 MW; 590889CEA55CC5EA CRC64;

Query Match 100.0%; Score 1858; DB 4; Length 345;

Best Local Similarity 100.0%; Pred. No. 4.1e-172;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSIFGLLLVTSALAGRRGTQAESNLSSKFQSSNKQNGVDPQHERIITVSTNGSIHS 60
 DB 1 MSIFGLLLVTSALAGRRGTQAESNLSSKFQSSNKQNGVDPQHERIITVSTNGSIHS 60
 QY 61 PRPHTYPRNTVLVRLVAEENVMQLTFDERFGLDEPDDICKYDFVEVEPSDGTIL 120
 DB 61 PRPHTYPRNTVLVRLVAEENVMQLTFDERFGLDEPDDICKYDFVEVEPSDGTIL 120
 QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFPPSEPGFCIHYNIVMPQTEAVSPVLPPSA 180
 DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFPPSEPGFCIHYNIVMPQTEAVSPVLPPSA 180
 QY 181 LPDLNNALTAFTSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240
 DB 181 LPDLNNALTAFTSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240
 QY 241 LTBVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
 DB 241 LTBVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
 QY 301 VTKYHEVLQRLPKTGVGRGLHKSITDVALEHHEECDCVCRGSGTG 345
 DB 301 VTKYHEVLQRLPKTGVGRGLHKSITDVALEHHEECDCVCRGSGTG 345

RESULT 2

Q9UL22 Q9UL22 PRELIMINARY; PRT; 345 AA.
 AC Q9UL22;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Secretory growth factor-like protein FALLOTEIN (SPINAL CORD-derived growth factor) (Platelet-derived growth factor C).
 GN RSCDGF OR PDGFC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RA Tsai Y.-J., Lee R.K.K., Lin S.P.;
 RT "Falloletin, a novel growth factor like gene identified in human uterus."
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Hamada T., Ui-Tei K., Miyata Y.;
 RT "A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family."
 RL FEBS Lett. 475:97-102(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21347863; PubMed=11297552;
 RA Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O., Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M., Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;
 RA "Platelet-derived Growth Factor C (PDGF-C), a Novel Growth Factor That Binds to PDGF alpha and beta Receptor."
 RT J. Biol. Chem. 276:27406-27414(2001).
 RL [3]
 CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL; AF091434; AAF00049.1; -.
 DR EMBL; AB033831; BAB03266.1; -.
 DR EMBL; AF260738; AAK51637.1; -.
 DR InterPro: IPR000859; CUB domain.
 DR InterPro: IPR000072; PD_Growth_factor.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00341; PDGF; 1.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00141; PDGF; 1.

DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS0278; PDGF; 2; 1.
 SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;
 Query Match 99.6%; Score 1851; DB 4; Length 345;
 Best Local Similarity 99.4%; Pred. No. 1.9e-171;
 Matches 343; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSIFGLLLVTSALAGRRGTQAESNLSSKFQSSNKQNGVDPQHERIITVSTNGSIHS 60
 DB 1 MSIFGLLLVTSALAGRRGTQAESNLSSKFQSSNKQNGVDPQHERIITVSTNGSIHS 60
 QY 61 PRPHTYPRNTVLVRLVAEENVMQLTFDERFGLDEPDDICKYDFVEVEPSDGTIL 120
 DB 61 PRPHTYPRNTVLVRLVAEENVMQLTFDERFGLDEPDDICKYDFVEVEPSDGTIL 120
 QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFPPSEPGFCIHYNIVMPQTEAVSPVLPPSA 180
 DB 121 GRWCGSGTVPKGQISKGNQIRIRFVSDEYFPPSEPGFCIHYNIVMPQTEAVSPVLPPSA 180
 QY 181 LPDLNNALTAFTSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240
 DB 181 LPDLNNALTAFTSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVGRKSRVVDLNL 240
 QY 241 LTBVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
 DB 241 LTBVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECCQVPSK 300
 QY 301 VTKYHEVLQRLPKTGVGRGLHKSITDVALEHHEECDCVCRGSGTG 345
 DB 301 VTKYHEVLQRLPKTGVGRGLHKSITDVALEHHEECDCVCRGSGTG 345
 RESULT 3
 Q9QY71 Q9QY71 PRELIMINARY; PRT; 345 AA.
 ID Q9QY71;
 AC Q9QY71;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Falloletin (Platelet-derived growth factor C).
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Tsai Y.-J., Lee R.K.K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;
 RT "cDNA cloning of falloletin from mouse ovary."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K., Gilbertson D., West J., O'Hara P.J.;
 RA "Platelet-derived growth factor C (PDGF-C), a novel growth factor that binds to PDGF alpha receptor."
 RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cacum, Cerebellum, and Head;
 RA MEDLINE=22354683; PubMed=12466851;
 RX The FANTOM Consortium,
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL; AF117608; AAF22516.1; -.
 DR EMBL; AF266467; AAK58566.1; -.
 DR EMBL; AK033734; BAC28455.1; -.

Wed Nov 26 13:03:31 2003

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DR EMBL; AK042767; BAC31358.1; -.
DR EMBL; AK052947; BAC35216.1; -.
DR MGI; MGI:1855631; Pdgfc_domain.
DR InterPro; IPR000859; CUB_growth_factor.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF; 2; 1.
DR PROSITE; PS02078; PDGF; 2; 1.
SQ SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84EA2 CRC64;

Query Match      89.6%; Score 1664; DB 11; Length 345;
Best Local Similarity 86.7%; Pred. No. 3e-153;
Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSLFGLLVTSALAGQRTGTAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MLLGLLLVTSALAGQRTGTAESNLSSKQLQSSDKQNGVQDPQHERVVTISNGSIHS 60

QY 61 PRFPHYPRNTVLVWRLVAVENWVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120
DB 61 PRFPHYPRNTVLVWRLVAVENWVQLTDFERFGLDEPDICKYDFVEVEEPSDGSVL 120

QY 61 PKFPHYPRNTVLVWRLVAVENWVQLTDFERFGLDEPDICKYDFVEVEEPSDGSVL 120
DB 61 PKFPHYPRNTVLVWRLVAVENWVQLTDFERFGLDEPDICKYDFVEVEEPSDGSVL 120

QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDYFPPSEPGFCIHYNIVMPQFTEAVSPSVLPSPA 180
DB 121 GRWCGSGTVPKGQISKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180

QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240

QY 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
DB 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300

QY 301 VTKEYHEVLQRPKTVGRLHLSLTDVALEHHEECDCVCRGSTG 345
DB 301 VTKEYHEVLQRPKTVGRLHLSLTDVALEHHEECDCVCRGNAGG 345

Query Match      89.6%; Score 1664; DB 11; Length 345;
Best Local Similarity 86.7%; Pred. No. 3e-153;
Matches 299; Conservative 28; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSLFGLLVTSALAGQRTGTAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MLLGLLLVTSALAGQRTGTAESNLSSKQLQSSDKQNGVQDPQHERVVTISNGSIHS 60

QY 61 PRFPHYPRNTVLVWRLVAVENWVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120
DB 61 PRFPHYPRNTVLVWRLVAVENWVQLTDFERFGLDEPDICKYDFVEVEEPSDGSVL 120

QY 61 PKFPHYPRNTVLVWRLVAVENWVQLTDFERFGLDEPDICKYDFVEVEEPSDGSVL 120
DB 61 PKFPHYPRNTVLVWRLVAVENWVQLTDFERFGLDEPDICKYDFVEVEEPSDGSVL 120

QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDYFPPSEPGFCIHYNIVMPQFTEAVSPSVLPSPA 180
DB 121 GRWCGSGTVPKGQISKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180

QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240

QY 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
DB 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300

QY 301 VTKEYHEVLQRPKTVGRLHLSLTDVALEHHEECDCVCRGSTG 345
DB 301 VTKEYHEVLQRPKTVGRLHLSLTDVALEHHEECDCVCRGNAGG 345

Query Match      89.5%; Score 1662; DB 11; Length 345;
Best Local Similarity 86.4%; Pred. No. 4.7e-153;
Matches 298; Conservative 29; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSLFGLLVTSALAGQRTGTAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MLLGLLLVTSALAGQRTGTAESNLSSKQLQSSDKQNGVQDPQHERVVTISNGSIHS 60

QY 61 PRFPHYPRNTVLVWRLVAVENWVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120
DB 61 PRFPHYPRNTVLVWRLVAVENWVQLTDFERFGLDEPDICKYDFVEVEEPSDGSVL 120

QY 61 PKFPHYPRNTVLVWRLVAVENWVQLTDFERFGLDEPDICKYDFVEVEEPSDGSVL 120
DB 61 PKFPHYPRNTVLVWRLVAVENWVQLTDFERFGLDEPDICKYDFVEVEEPSDGSVL 120
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QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDYFPPSEPGFCIHYNIVMPQFTEAVSPSVLPSPA 180
DB 121 GRWCGSGTVPKGQISKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180

QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240

QY 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
DB 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300

QY 301 VTKEYHEVLQRPKTVGRLHLSLTDVALEHHEECDCVCRGSTG 345
DB 301 VTKEYHEVLQRPKTVGRLHLSLTDVALEHHEECDCVCRGNAGG 345

Query Match      88.6%; Score 1646; DB 11; Length 345;
Best Local Similarity 85.5%; Pred. No. 1.7e-151;
Matches 295; Conservative 30; Mismatches 20; Indels 0; Gaps 0;

QY 1 MSLFGLLVTSALAGQRTGTAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MLLGLLLVTSALAGQRTGTAESNLSSKQLQSSDKQNGVQDPQHERVVTISNGSIHS 60

QY 61 PRFPHYPRNTVLVWRLVAVENWVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120
DB 61 PRFPHYPRNTVLVWRLVAVENWVQLTDFERFGLDEPDICKYDFVEVEEPSDGSVL 120

QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDYFPPSEPGFCIHYNIVMPQFTEAVSPSVLPSPA 180
DB 121 GRWCGSGTVPKGQISKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180

QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240

QY 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
DB 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300

Query Match      88.6%; Score 1646; DB 11; Length 345;
Best Local Similarity 85.5%; Pred. No. 1.7e-151;
Matches 295; Conservative 30; Mismatches 20; Indels 0; Gaps 0;

QY 1 MSLFGLLVTSALAGQRTGTAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
DB 1 MLLGLLLVTSALAGQRTGTAESNLSSKQLQSSDKQNGVQDPQHERVVTISNGSIHS 60

QY 61 PRFPHYPRNTVLVWRLVAVENWVQLTDFERFGLDEPDICKYDFVEVEEPSDGTIL 120
DB 61 PRFPHYPRNTVLVWRLVAVENWVQLTDFERFGLDEPDICKYDFVEVEEPSDGSVL 120

QY 121 GRWCGSGTVPKGQISKGNQIRIRFVSDYFPPSEPGFCIHYNIVMPQFTEAVSPSVLPSPA 180
DB 121 GRWCGSGTVPKGQISKGNHIRIRFVSDYFPPSEPGFCIHYSIIMPQVTTTSPSVLPSS 180

QY 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240
DB 181 LPDLLNNAITAFSTLEDLIRYLEPERWQDLEDLYRPTWQLLGKAFVFGKSRVVDLNL 240

QY 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
DB 241 LEEVRLYSCPTPRNFVSISREELKRTDTIFWPGCLLVKRCGNCACCLHNCNECQVPSK 300
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Db 241 LKEVKLYSCTPRNFSVIREELKRTDTTFWPGLLVKRCGNCACCLHNCNECQCVPK 300
QY 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHECDVCVCGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHECDVCVCGSTGG 345

RESULT 6
Q9JHV8 PRELIMINARY; PRT; 345 AA.
AC Q9JHV8
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Platelet-derived growth factor C.
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss-Webster/NIH;
EX MEDLINE=20417814; PubMed=10960785;
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
RT "The mouse Pdgfc gene: dynamic expression in embryonic tissues during
organogenesis.";
RL Mech. Dev. 96:209-213 (2000).
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AF286725; AAF91483.1; -.
DR MGD; MGI:1859631; Pdgfc.
DR InterPro; IPR000859; CUB_domain.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; PDGF; 1.
DR PROSITE; PS0278; PDGF 2; 1.
SQ SEQUENCE 345 AA; 3886 MW; FA1486BED6D362F8 CRC64;

Query Match 88.0%; Score 1635; DB 11; Length 345;
Best Local Similarity 85.5%; Pred. No. 2e-150;
Matches 295; Conservative 28; Mismatches 22; Indels 0; Gaps 0;

QY 1 MSLFGLLLTSALAGQRTQAESNLSSKQFQSSNKEQGVQDPQHERIITVSTNGSIHS 60
Db 1 MLLGLLLTSALAGQRTQAESNLSSKQFQSSNKEQGVQDPQHERIITVSTNGSIHS 60
QY 61 PRPHTYPRNTVLVWRLVAEENVMQLTFDERFGLDEPDDICKYDFVEVEPSPDGTIL 120
Db 61 PRPHTYPRNTVLVWRLVAEENVMQLTFDERFGLDEPDDICKYDFVEVEPSPDGTIL 120
QY 121 GRWCGSGTVPGKQISKGNIQIRIRFVSDEYFPSPGFCIHYNIVMPQTEAVSPSVLPSPA 180
Db 121 GRWCGSETVPGKQISKGNIQIRIRFVSDEYFPSPGFCIHYSIIMPVTTTSFSLPSS 180
QY 181 LPDLINNAITASTLEDLIRYLEPERWQDLDELXRPWTQLGKAFVGRKSRVVDNL 240
Db 181 LSLDLINNAITASTLEDLIRYLEPERWQDLDELXRPWTQLGKAFVYKSKVVDNL 240
QY 241 LTEEVRLYSCTPRNFSVIREELKRTDTTFWPGLLVKRCGNCACCLHNCNECQCVPK 300
Db 241 LKEVKLYSCTPRNFSVIREELKRTDTTFWPGLLVKRCGNCACCLHNCNECQCVPK 300
QY 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHECDVCVCGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHECDVCVCGSTGG 345

RESULT 7
Q9I946 PRELIMINARY; PRT; 345 AA.
AC Q9I946

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DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE Spinal cord-derived growth factor.
GN SCDGF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=Spinal cord;
EX MEDLINE=20317014; PubMed=10858496;
RA Hamada T., Ui-Tei K., Miyata Y.;
RT "A novel gene derived from developing spinal cords, SCDGF, is a unique
member of the PDGF/VEGF family.";
RL FEBS Lett. 475:97-102 (2000).
CC -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB033829; BAB03265.1; -.
DR InterPro; IPR000859; CUB_domain.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00341; PDGF; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS0278; PDGF 2; 1.
SQ SEQUENCE 345 AA; 38940 MW; 97ACEA992BF5128C CRC64;

Query Match 86.9%; Score 1614; DB 13; Length 345;
Best Local Similarity 83.8%; Pred. No. 2.2e-148;
Matches 289; Conservative 31; Mismatches 25; Indels 0; Gaps 0;

QY 1 MSLFGLLLTSALAGQRTQAESNLSSKQFQSSNKEQGVQDPQHERIITVSTNGSIHS 60
Db 1 MLLGLLLTSALAGRRHGAARSDLSKFSFGAKQGVQDPQHEKIITVTSNGSIHS 60
QY 61 PRPHTYPRNTVLVWRLVAEENVMQLTFDERFGLDEPDDICKYDFVEVEPSPDGTIL 120
Db 61 PRPHTYPRNTVLVWRLVAEENVMQLTFDERFGLDEPDDICKYDFVEVEPSPDGTIL 120
QY 121 GRWCGSGTVPGKQISKGNIQIRIRFVSDEYFPSPGFCIHYNIVMPQTEAVSPSVLPSPA 180
Db 121 GRWCGSSVSPSRQISKGNIQIRIRFVSDEYFPSPGFCIHYNIVMPQTEAVSPSVLPSPA 180
QY 181 LPDLINNAITASTLEDLIRYLEPERWQDLDELXRPWTQLGKAFVGRKSRVVDNL 240
Db 181 LPDLINNAITASTLEDLIRYLEPERWQDLDELXRPWTQLGKAFVGRKSRVVDNL 240
QY 241 LTEEVRLYSCTPRNFSVIREELKRTDTTFWPGLLVKRCGNCACCLHNCNECQCVPK 300
Db 241 LKEEVRLYSCTPRNFSVIREELKRTDTTFWPGLLVKRCGNCACCHQNCQCQIPTK 300
QY 301 VTKKYHEVLQRPKTVGRGLHSLTDVALEHHECDVCVCGSTGG 345
Db 301 VTKKYHEVLQRPKTVGRGLHSLTDVPLEHHECDVCVCGSTGG 345

RESULT 8
Q8K429 PRELIMINARY; PRT; 258 AA.
ID Q8K429
AC Q8K429
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Platelet-derived growth factor C (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=Sprague-Dawley; TISSUE=Skin;
RA Brown S.A., Coberly D.M., Rohrich R.R., Chao J.J.;
RT "Platelet Derived Growth Factor C (PDGF-C) Expression in Wound
Healing."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AF508348; AAM47265.1; -
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000072; PD_Growth_factor.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF_2; 1.
FT NON_TER 258
FT NON_TER 258
SQ SEQUENCE 258 AA; 29255 MW; 88625B989FC3F8B CRC64;

Query Match 67.8%; Score 1260; DB 11; Length 258;
Best Local Similarity 85.6%; Pred. No. 3.9e-114;
Matches 220; Conservative 25; Mismatches 12; Indels 0; Gaps 0;

QY 42 QDQHERIITVSTNGSIHSPRPHTYPRNTVLVWELVAEENVMQLTFDERFGLDEPED 101
Db 1 QDQHERVITSGNSIHSKPKPHTYPRNTVLVWELVAEENVMQLTFDERFGLDEPED 60

QY 102 DICKYDFVEVEBPSTGILGRWCGSGTVPKGQISKGNQIRIRFVSDYFPPSPGFCIHYN 161
Db 61 DICKYDFVEVEBPSTGILGRWCGSGTVPKGQISKGNHIRIRFVSDYFPPSPGFCIHYN 120

QY 162 IVMQFTRAVSPSVLPSPALPDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLRYPTWQ 221
Db 121 IIMQVTTSTSPVLPSPALSLLNNAITAFSTVEELIRFLEPDWQIDLSLYKPTWP 180

QY 222 LLGKAFVGRKRVVDNLLTEVRLYSCTPNFSVIREELKRTDTIEMPGCLLVKRCG 281
Db 181 LLGKAFVGRKRVVDNLLTEVRLYSCTPNFSVIREELKRTDTIEMPGCLLVKRCG 240

QY 282 GNCACCLHNCNQCQVP 298
Db 241 GNCACCLHNCNQCQVP 257

RESULT 9
Q9GZP0 PRELIMINARY; PRT; 370 AA.
AC Q9GZP0; 01-WAR-2001 (TrEMBLrel. 16, Created)
DT 01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SPINAL CORD-derived growth factor-B (MSTP036) (IRIS-expressed growth
factor long form) (Platelet-derived growth factor D).
GN HSCDGF-B OR IEGF OR PDGFD.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamada I., Ui-Tei K., Imaki J., Miyata Y.;
RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to
SCDGF/PPGF-C/fallotsein."
RL Biochem. Biophys. Res. Commun. 0:0-0 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RA Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
RA Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
RA Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
RA Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Iris;

RA Wistow G.;
RT "Iris-expressed Growth Factor (IEGF).";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC [4]
RP SEQUENCE FROM N.A.
RX PubMed-11331881;
RA Bergsten E., Urcela M., Li X., Pietras K., Ostman A., Heidin C.H.,
RA Alitalo K., Eriksson U.;
RA "PDGF-D is a specific, protease-activated ligand for the PDGF beta-
receptor."
RT Nat. Cell Biol. 3:512-516 (2001).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE-21231380; PubMed-11331882;
RA LaRoche W.J., Jeffers M., McDonald W.F., Chillakuru R.A.,
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
RA Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shinkets J.,
RA Shinkets R.A., Rothberg J.M., Lichenstein H.S.;
RT "PDGF D, A Novel Protease-Activated Growth Factor."
RL Nat. Cell Biol. 3:517-521 (2001).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL; AB033832; BAB18903.1; -
DR EMBL; AF113216; AAG39287.1; -
DR EMBL; AY027517; AAK20081.1; -
DR EMBL; AF336376; AAK56136.1; -
DR EMBL; AF335584; AAK38840.1; -
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000072; PD growth factor.
DR InterPro; IPR000531; TonB_boxC.
DR Pfam; PF00431; CUB; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS02078; PDGF_2; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
SQ SEQUENCE 370 AA; 42584 MW; D387F485E7BB7674 CRC64;

Query Match 39.9%; Score 741.5; DB 4; Length 370;
Best Local Similarity 43.6%; Pred. No. 1.6e-63;
Matches 159; Conservative 59; Mismatches 114; Indels 33; Gaps 10;

QY 3 LFGLLIVTSALAGQRGTQAEENLSKQFSSN---KEONGVOD-POHERIITVSTNGSI 58
Db 5 IFVYTHICANFCSDRTSATPOSASIKALRNAMLRDENHLLTDLRRDETQVKGNGYV 64

QY 59 HSPRPHTYPRNTVLVWELVAEENVMQLTFDERFGLDEPEDDICKYDFVEVEBPSDGT 118
Db 65 QSPRFNSYPRNLLTWRLHS-QENTRIQLVFDNQFGLSEAENDICKYDFVEVEDSETS 123

QY 119 --ILGRWCGSGTVPKGQISKGNQIRIRFVSDYFPPSPGFCIHYNVMQFTEAV---- 171
Db 124 TIIRGERWCGHKEVPPRIKSRNTNQIKITFKSDDYFVAKPGPKIYYSL-LEDQFAAASETN 182

QY 172 -----SPSVLPSPALPDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLIR 217
Db 183 WESVTSSISGVSYNSFSVTDPT-LIADALDKKTAEDTVEDLLKYFNFSQESQEDLENNYL 241

QY 218 PTWQLLGKAFVGRKRVVDNLLTEVRLYSCTPNFSVIREELKRTDTIEMPGCLLV 277
Db 242 DTPRYGRSY-HDRKSK-VDLRLNDLDAKRYSCTPNYSVNIIEELKLANVVPFPCLLV 299

QY 278 KRCGNCACCLHNCNQCQVPKVKYKHEVLQIRP---KTGVRGLHKSITDVALEHHEE 334
Db 300 QRCGNCGCGTGVNWRSCNCGTKVTKYKHEVLQIRP---KTGVRGLHKSITDVALEHHEE 359

335 CDCVC 339
360 CDCIC 364

RESULT 10
Q9BWV5 PRELIMINARY; PRT; 364 AA.
ID Q9BWV5

AC Q9BWV5; 2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Iris-expressed growth factor short form (Spinal cord-derived growth factor-B).
 DE factor-B).
 GN IEGF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=iris;
 RC Tissue=iris;
 RA Wistow G.;
 RT "Iris-expressed Growth Factor (IEGF).";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Tissue=Testis;
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY027518; AAK20082.1; -;
 DR EMBL; BC030645; AAH30645.1; -;
 DR InterPro; IPR000859; CUB domain.
 DR InterPro; IPR000072; PD growth factor.
 DR InterPro; IPR000531; TonB_boxC.
 DR Pfam; PF00431; CUB; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS02078; PDGF 2; 1.
 DR PROSITE; PS00430; TONB DEPENDENT REC 1; 1.
 SQ SEQUENCE 364 AA; 42166 MW; 245C53E8DDEA9EAC CRC64;
 Query Match 39.9%; Score 740.5; DB 4; Length 364;
 Best Local Similarity 43.2%; Pred. NO. 2e-63;
 Matches 156; Conservative 61; Mismatches 113; Indels 31; Gaps 9;
 QY 3 LFGLLVTSALAGQRRGTOAESNLSSKQFSSNKEQGVDPQHERIITVSTNGSIHSPR 62
 DB 5 IFVYLLICANFCSCRTSATPQASIKALRNANLRDDLY--RRDETIOVKNGYVQSPR 62
 QY 63 FHTYPRNTVLVRLVAVENVMQITFEDRFGLEDPEDDICKYDFVEVEPESDGT--IL 120
 DB 63 FPNYPRNLLTWLHS--QENTRIQLVFNQFQLEAEANDICRYDFVEVEDISSTIIR 121
 QY 121 GRWCGSGTPGCKOISKNQIRIRFVSDEYPPSPGCIHYNVMPQFTEAV----- 171
 DB 122 GRWCGHKEVPPRIKSRNQIKITFKSDDYFVAKPGFIYSL--LEDQPAAASGTWESV 180
 QY 172 -----SPSLVPPSALPLDLNNAITAFSTLEDLIRYLEPRWQLDLEDLYRPTWQ 221
 DB 181 TSSISGVSYNSPVTDP--LIADALDKKIAEFDTVEDLLKYPNPSWQEDLENNYLDTPR 239
 QY 222 LIGKAFVFGKSRVDNLLTTEVRLYSCTPRFSVIRELKTDTIIFWPGCLLYKRCG 281
 DB 240 YRGRSY-HDRKSK-VLDRLNDKAKRYSCTPRYSVNIREFLKVNVFPRCLLVQRCG 297
 QY 282 GNCACCLHNCQCVPSKTKYHVLQLRP---KTGVRGLHKLTDVALEHHECDVCV 338
 DB 298 GNCGCGTGNWNRSTCNCGTKVKKYHVLQEPGHKRGRAKTNALVDIQLDHHRCDCI 357
 QY 339 C 339
 DB 358 C 358
 RESULT 11
 Q92517 PRELIMINARY; PRT; 370 AA.
 ID Q92517; Q92517;
 AC Q92517; Q92517;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE platelet-derived growth factor D (18-day embryo whole body cdna, RIKEN full-length enriched library, clone:1110003109 product:platelet-derived growth factor D).
 GN PDGFD.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/C;
 RC MEDLINE=21231380; PubMed=11331882;
 RA LaRoche W.J., Jeffers M., McDonald W.F., Chillakuru R.A., Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C., Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J., Shimkets R.A., Rothberg J.M., Lichtenstein H.S.;
 RA "PDGF D, A Novel Protease-Activated Growth Factor.";
 RT Nat. Cell Biol. 3:517-521(2001).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanegaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai T., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
 RA Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RC MEDLINE=22354693; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RC MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RC MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RC MEDLINE=20493374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RA "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RC MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,


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Qy 133 QISKGNIQIRIRFVSDYFSEPGFCIHYNIVMPQFTEAV-----SPS 174
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 140 ITSKTQIKITFKSDDYFAKPGFKIYVSDSQEAASETNWESVTSFSGSVYHSDS 199
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 175 VLPSALPLDLNNATATSTLEDLYLEPERWQOLDLEDYRPTWQLLGKAFVGRKSR 234
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 200 ITDPT-LTADALDKTVAEFDTVEDLLKHFNPSWQDDLENLYLDTPHYGRSY-HDRKSK 257
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 235 VVDL 238
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 258 GIEV 261

RESULT 14
Q8QFX6 PRELIMINARY; PRT; 923 AA.
AC Q8QFX6;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Neuropilin-1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee P., Goishi K., Davidson A., Mannix R., Zon L., Klagsbrun M.;
RT "Neuropilin-1 is required for normal vascular development and is a
RT mediator of VEGF-dependent angiogenesis in zebrafish."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
DR EMBL; AY064213; AAL40862.1; -.
DR InterPro; IPR000859; CUB domain.
DR InterPro; IPR000421; FA58_C.
DR InterPro; IPR000998; MAM_domain.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00754; F5_F8_type_C; 2.
DR Pfam; PF00629; MAM; 1.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00231; FA58C; 2.
DR SMART; SMC0137; MAM; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01285; FA58C_1; 1.
DR PROSITE; PS01286; FA58C_2; 2.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS00660; MAM_2; 1.
KW Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 923 AA; 102492 MW; 2ED84B129AA92B2D CRC64;

Query Match 10.3%; Score 190.5; DB 13; Length 923;
Best Local Similarity 27.6%; Pred. No. 2.1e-09;
Matches 66; Conservative 29; Mismatches 95; Indels 49; Gaps 8;

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Db 12 GIFLIVSALKNDKCGDN-----IRITSANYLTSPGYP 43
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Qy 65 HTYPRNTVLVRLVAEENWVQLTFDERFGLDEPDDICKYDFVEVEEPPSD--GTILGR 122
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Db 157 KSPGPFKEKYPNNLDCTFMIFAPKMSIIVLEFESFELEPDTQP-----PAGVFCRYDL 209
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Search completed: November 25, 2003, 21:04:33
Job time : 31.4613 secs

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Db 157 KSPGPFKEKYPNNLDCTFMIFAPKMSIIVLEFESFELEPDTQP-----PAGVFCRYDL 209
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RESULT 15
Q8AXP1 PRELIMINARY; PRT; 923 AA.
AC Q8AXP1;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Neuropilin-1.
GN NP-1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Shoji W., Tawarayama H.;
RT "The cloning and expression of neuropilin-1."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB098776; BAC3657.1; -.
SQ SEQUENCE 923 AA; 102541 MW; 0E6CE33ED28A21F7 CRC64;

Query Match 10.3%; Score 190.5; DB 13; Length 923;
Best Local Similarity 27.6%; Pred. No. 2.1e-09;
Matches 66; Conservative 29; Mismatches 95; Indels 49; Gaps 8;

Qy 5 GLLIVTSALAGQRRGTQAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRP 64
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Search completed: November 25, 2003, 21:04:33
Job time : 31.4613 secs

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GenCore version 5.1.6
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QM nucleic - nucleic search, using sw model

Run on: November 25, 2003, 22:28:25 ; Search time 3795.28 Seconds
(without alignments)
16556.656 Million cell updates/sec

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Perfect score: 1536
Sequence: 1 cgggtaattccagttttcc.....tgctgataggacagactgga 1536

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2988711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_on.*
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- 6: gb_pat.*
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- 15: em_ba.*
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- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Prei. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1532.6	99.8	2825	6 AR210624	AR210624 Sequence
2	1532.6	99.8	2825	6 AR232022	AR232022 Sequence
3	1532.6	99.8	2849	6 AX047650	AX047650 Sequence
4	1532.6	99.8	2849	6 AX391260	AX391260 Sequence
5	1532.6	99.8	2849	6 AX464152	AX464152 Sequence
6	1532.2	99.8	2152	9 AF244813	AF244813 Homo sapi
7	1531	99.7	3007	9 AF234498	AF234498 Sequence
8	1531	99.7	3007	9 AF091434	AF091434 Homo sapi
9	1511.8	98.4	1804	6 AX739931	AX739931 Sequence
10	1511.8	98.4	1804	9 AF260738	AF260738 Homo sapi
11	1511	98.4	1760	6 AR267280	AR267280 Sequence
12	1511	98.4	1760	6 AR282949	AR282949 Sequence
13	1511	98.4	1760	6 AX044518	AX044518 Sequence
14	1511	98.4	1760	6 AX118785	AX118785 Sequence
15	1352.6	88.1	1817	9 AB033831	AB033831 Homo sapi
16	1149	74.8	1328	6 BD004757	BD004757 Novel VRG
17	1149	74.8	1328	6 BD168832	BD168832 Antibody
18	955.6	62.2	1095	6 AR282992	AR282992 Sequence
19	952.6	62.0	1035	6 AX027935	AX027935 Sequence
20	721	46.9	3512	10 AF266467	AF266467 Mus muscu
21	721	46.9	3571	6 AR267281	AR267281 Sequence
22	721	46.9	3571	6 AR282985	AR282985 Sequence
23	721	46.9	3571	6 AX044520	AX044520 Sequence
24	721	46.9	3571	6 AX118787	AX118787 Sequence
25	719.4	46.8	2692	10 AF117608	AF117608 Mus muscu
26	717.2	46.7	1116	10 AB033830	AB033830 Rattus no
27	716.2	46.6	2731	10 BC037696	BC037696 Mus muscu
28	710.2	46.2	1038	10 AF286725	AF286725 Mus muscu
29	704.2	45.8	1675	5 AB033829	AB033829 Gallus ga
30	694.4	45.2	196952	9 AC092608	AC092608 Homo sapi
31	684.4	44.6	1035	6 AR282950	AR282950 Sequence
32	621	40.4	918	6 AX119274	AX119274 Sequence
33	574.6	37.4	774	10 AF508348	AF508348 Rattus no
34	431	28.1	504	6 AX027960	AX027960 Sequence
35	331.4	21.6	82113	2 AC015451	AC015451 Homo sapi
36	287	18.7	300	6 AX027962	AX027962 Sequence
37	287	18.7	300	6 AX027981	AX027981 Sequence
38	284	18.5	284	6 AX027963	AX027963 Sequence
39	284	18.5	284	6 AX027982	AX027982 Sequence
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41	283.4	18.5	289	6 AX027993	AX027993 Sequence
42	278.6	18.1	279	6 AX027968	AX027968 Sequence
43	278.6	18.1	279	6 AX027989	AX027989 Sequence
44	273	17.8	275	6 AX027964	AX027964 Sequence
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ALIGNMENTS

RESULT 1	AR210624	AR210624	2825 bp	DNA	linear	PAT 20-JUN-2002
LOCUS	Sequence 1	from patent US 6391311.				
DEFINITION	Sequence 1	from patent US 6391311.				
ACCESSION	AR210624					
VERSION	AR210624.1	GI:21513401				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 2825)					
AUTHORS	Ferrara, N. and Kuo, S.S.					
TITLE	Polypeptides having homology to vascular endothelial cell growth factor and bone morphogenetic protein 1					
JOURNAL	Patent: US 6391311-A 1 21-MAY-2002;					

FEATURES		Location/Qualifiers		1..2825		/organism="unknown"		849 a		522 c		605 g		848 t		1 others	
source																	
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ORIGIN																	
Query Match		99.8%;		Score 1532.6;		DB 6;		Length 2825;									
Best Local Similarity		99.9%;		Pred. No. 0;													
Matches 1532;		Conservative		1;		Mismatches		0;		Indels		0;		Gaps		0;	
Qy	4	GTAAATTCAGTTCCTCCAGCAACAAAGAAACGAGTCAAGATCTCCAGCATGAGA		63													
Db	341	GTAAATTCAGTTCCTCCAGCAACAAAGAAACGAGTCAAGATCTCCAGCATGAGA		400													
Qy	64	GAATTTACTGTCCTACTAATGAAGTATTCACAGCCCAAGTTCCTCATATCTATC		123													
Db	401	GAATTTACTGTCCTACTAATGAAGTATTCACAGCCCAAGTTCCTCATATCTATC		460													
Qy	124	CAAGAAATACGCTCTTGGTATCGAGATTAGTACGAGTACAGGAAATATGATGATCAAC		183													
Db	461	CAAGAAATACGCTCTTGGTATCGAGATTAGTACGAGTACAGGAAATATGATGATCAAC		520													
Qy	184	TTACGTTTGAAGAAAGATTGGCTTGAAGACCAAGAAATGACATATGCAAGTATGATT		243													
Db	521	TTACGTTTGAAGAAAGATTGGCTTGAAGACCAAGAAATGACATATGCAAGTATGATT		580													
Qy	244	TTGTAGAAATGAGGAAACCAAGTATGAGTATGAGTATGAGTATGAGTATGAGTATG		303													
Db	581	TTGTAGAAATGAGGAAACCAAGTATGAGTATGAGTATGAGTATGAGTATGAGTATG		640													
Qy	304	CTGTACCAAGAAACAGATTTCTAAAGGAAATCAAAATAGGATTAAGATTTGATCTGATG		363													
Db	641	CTGTACCAAGAAACAGATTTCTAAAGGAAATCAAAATAGGATTAAGATTTGATCTGATG		700													
Qy	364	AATATTTCTCTGAGCAAGGTTCTGATCACTACCAATGTCATGATGTCATGATGTCATG		423													
Db	701	AATATTTCTCTGAGCAAGGTTCTGATCACTACCAATGTCATGATGTCATGATGTCATG		760													
Qy	424	CAGAGCTGTAGTCTCTGATGCTACCCCTTACCTTACCTTACCTTACCTTACCTTACCT		483													
Db	761	CAGAGCTGTAGTCTCTGATGCTACCCCTTACCTTACCTTACCTTACCTTACCTTACCT		820													
Qy	484	ATGCTTAATCTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCAAGAGAT		543													
Db	821	ATGCTTAATCTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCAAGAGAT		880													
Qy	544	GGCAGTTGGACTTAGAAGATCTATATAGGCACTTGGCACTTCTTGGCAAGCTTTTG		603													
Db	881	GGCAGTTGGACTTAGAAGATCTATATAGGCACTTGGCACTTCTTGGCAAGCTTTTG		940													
Qy	604	TTTTTGGAGAAATCCAGAGTGTGATCTGAACCTTCTAAACAGAGGAGTAAAGATTAT		663													
Db	941	TTTTTGGAGAAATCCAGAGTGTGATCTGAACCTTCTAAACAGAGGAGTAAAGATTAT		1000													
Qy	664	ACAGCTGCACACCTCGTAACTTCTAGTGTCCATTAAGGAAAGAACTTAAAGAACCGATA		723													
Db	1001	ACAGCTGCACACCTCGTAACTTCTAGTGTCCATTAAGGAAAGAACTTAAAGAACCGATA		1060													
Qy	724	CAATTTCTGCGCAGGTTGCTCTCGTTTAAACGCTGTGTGGGAACTGTGCTGTGTC		783													
Db	1061	CAATTTCTGCGCAGGTTGCTCTCGTTTAAACGCTGTGTGGGAACTGTGCTGTGTC		1120													
Qy	784	TCCAAATTCGAATGAATGTCAATGTCTCCCAAGCAAAAGTTACTTAAAAAAATCCACGAGG		843													
Db	1121	TCCAAATTCGAATGAATGTCAATGTCTCCCAAGCAAAAGTTACTTAAAAAAATCCACGAGG		1180													
Qy	844	TCCTTCAGTTGAGACCAAAACCCGGTGTCCAGGGATTGCAAAATCTCACCGACGTGG		903													
Db	1181	TCCTTCAGTTGAGACCAAAACCCGGTGTCCAGGGATTGCAAAATCTCACCGACGTGG		1240													
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RESULT 2	AR232022	LOCUS	Sequence 1 from patent US 6455283.	2825 bp	DNA	linear	PAT 20-DEC-2002
DEFINITION	AR232022	ACCESSION	AR232022	GI:27273902			
KEYWORDS	Unknown.	ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 2825)	AUTHORS	Ferrara, N. and Kuo, S.S.				
TITLE	Nucleic acids encoding vascular endothelial cell growth factor-E (VEGF-E)	JOURNAL	Patent: US 6455283-A 1 24-SEP-2002;				
FEATURES	source	1..2825	/organism="unknown"	848 t	1 others		
BASE COUNT	849 a	522 c	605 g				
ORIGIN							
Query Match	99.8%;	Score 1532.6;	DB 6;	Length 2825;			
Best Local Similarity	99.9%;	Pred. No. 0;					
Matches 1532;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps
Qy	4	GTAAATTCAGTTCCTCCAGCAACAAAGAAACGAGTCAAGATCTCCAGCATGAGA		63			
Db	341	GTAAATTCAGTTCCTCCAGCAACAAAGAAACGAGTCAAGATCTCCAGCATGAGA		400			
Qy	64	GAATTTACTGTCCTACTAATGAAGTATTCACAGCCCAAGTTCCTCATATCTATC		123			

Db 401 GAAATATTACTGTGTCTACTAATGAAGATATTACAGCCCAAGGTTTCTCATCATATTATC 460
Qy 124 CAAGAAATACCGTCTTGGTATGCGAGATTAGTAGCAGTAGTAGAGAAATGTATGATACAAAC 183
Db 461 CAAGAAATACCGTCTTGGTATGCGAGATTAGTAGCAGTAGTAGAGAAATGTATGATACAAAC 520
Qy 184 TTACCTTTTGATGAAGAATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTAGTATT 243
Db 521 TTACCTTTTGATGAAGAATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTAGTATT 580
Qy 244 TTGTAGAAATGAGAAACCCAGTAGTGAACATATATTAGGGCGCTGGTGGTCTTGTA 303
Db 581 TTGTAGAAATGAGAAACCCAGTAGTGAACATATATTAGGGCGCTGGTGGTCTTGTA 640
Qy 304 CTGTACCAAGGAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTGTATCTGATG 363
Db 641 CTGTACCAAGGAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTGTATCTGATG 700
Qy 364 AATATTTTCTCTGAAACAGGGTTCTGCATCCACTACAACTATGTCATGCCAATTC 423
Db 701 AATATTTTCTCTGAAACAGGGTTCTGCATCCACTACAACTATGTCATGCCAATTC 760
Qy 424 CAGAGCTGTAGTCTTCACTGCTACCCCTTCACTTGGCACTGGACCTGCTTAATA 483
Db 761 CAGAGCTGTAGTCTTCACTGCTACCCCTTCACTTGGCACTGGACCTGCTTAATA 820
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Qy 724 CAATTTCTGGCAGGTTGTCTCTGTAAACGCTGTGGTGGGAACCTGTGCTGTGTGTC 783
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ACCESSION AX047650.1 GI:11876693
VERSION
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Chen, J., Ferrara, N., Fong, S., Goddard, A., Gurney, A.L.,
Hillan, K.J., Kuo, S.S., Tumas, D. and Wood, W.I.
TITLE Compositions and methods for the treatment of immune related
diseases
JOURNAL Patent: WO 0070050-A 9 23-NOV-2000;
Genentech, Inc. (US)
FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
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unsure
BASE COUNT 851 a 528 c 619 g 850 t 1 others
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Li, X., Ponten, A., Aase, K., Karlsson, L., Abramson, A., Uutela, M.,
Backstrom, G., Hellstrom, M., Bostrom, H., Li, H., Soriano, P.,
Besholtz, C., Heldin, C.-H., Allitala, K., Ostman, A. and Eriksson, U.
PDGF-C is a new protease-activated ligand for the PDGF
alpha-receptor
Nat. Cell Biol. 2 (5), 302-309 (2000)
JOURNAL Nat. Cell Biol. 2 (5), 302-309 (2000)
MEDLINE 20268201
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REFERENCE 2 (bases 1 to 2152)
Eriksson, U., Aase, K., Li, X. and Ponten, A.
AUTHORS Direct Submission
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DEFINITION AX234498
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VERSION AX234498.1 GI:15593481
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ORGANISM Homo sapiens
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REFERENCE
1 Alitalo, K.M. and Jeltsch, M.M.
Materials and methods involving hybrid vascular endothelial growth
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JOURNAL LUDWIG INSTITUTE FOR CANCER RESEARCH (US) ; Licentia OY (FI)
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1136 CCCTGGAGCACCATGAGAGTGTGACTGTGTGTCAGAGGGAGCAAGGAGTAGCCG 1195
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964 ATCAACACAGCAGCTCTTGCCAGAGCTGTGCAAGTGTGCTGATTTCTATTAGAGAA 1023
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Db
1196 ATCAACACAGCAGCTCTTGCCAGAGCTGTGCAAGTGTGCTGATTTCTATTAGAGAA 1255
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1736 TTAACCTTTGTGTCGCTGATAGA 1760
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RESULT 12
LOCUS AR282949 1760 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1 from patent US 6528050.
ACCESSION AR282949
VERSION AR282949.1 GI:29719770
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1760)
AUTHORS Gao,Z., Hart,C.E., Piddington,C.S., Sheppard,P.O., Shoemaker,K.E.,
Gilbertson,P.G. and West,J.W.
TITLE Growth factor homolog zvegfg3
JOURNAL Patent: US 6528050-A 1 04-MAR-2003;
FEATURES Location/Qualifiers
source 1. 1760
BASE COUNT 494 a 373 c 411 g 482 t
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Query Match 98.4%; Score 1511; DB 6; Length 1760;
Best Local Similarity 99.8%; Pred. No. 0;
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Qy 1443 AACCAGAACATCTATGTACTACAAACCTGGTTTTTAAAGAGAACTATGTTGCTATGAA 1502
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RESULT 14
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LOCUS AX118785 1760 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 1 from Patent WO0128586.
ACCESSION AX118785

AX118785.1 GI:14035734
Homo sapiens (human)
Homo sapiens
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
1
Gilbertson,D.G.
Method of treating fibrosis
Patent: WO 0128586-A.1 26-APR-2001;
Zymogenetics, Inc. (US)
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BASE COUNT
ORIGIN
Query Match 98.4%; Score 1511; DB 6; Length 1760;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1522; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
Qy 4 GTAAATTCAGTCTTTCAGCAACAAAGGAAACAGAACGGAGTACAGATCCTCAGCATGAGA 63
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1384	CCCTAAATCCGTATTAATCTGGGA-TTTTTTTTTTTTTTTTTTTTTTTTGTCTCATATTACATATGTA	1442
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RESULT 15	AB033831	1917 bp	linear	PRI 26-JUL-2000
LOCUS	AB033831			
DEFINITION	Homo sapiens hSCGF mRNA for spinal cord-derived growth factor, complete cds.			
ACCESSION	AB033831			

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 25, 2003, 22:26:15 ; Search time 283.611 Seconds
(without alignments)
14619.814 Million cell updates/sec

Title: US-09-852-209a-4

Perfect score: 1536

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Human VEGF-E DNA.
DNA encoding human
Human PRO200 nucle
Human PRO200 (UNQ1
Human PRO200 (VEGF
Human PRO200 prote
Human PRO713 CDNA

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13	1532.6	99.8	2849	25	AAZ03745	CDNA encoding huma
14	1532.6	99.8	2849	25	AAZ04166	Human CDNA encodin
15	1532.6	99.8	2849	25	AAZ89283	DNA encoding novel
16	1532.6	99.8	2849	25	AAZ92668	CDNA encoding huma
17	1532.2	99.8	2108	21	AAA12523	CDNA encoding plat
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19	1531	99.7	2839	21	AAZ47452	Human TANGO 128 co
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21	1531	99.7	3007	22	AAZ12884	DNA encoding for h
22	1529.4	99.6	2779	21	AAZ52458	CDNA encoding huma
23	1521.6	99.1	2632	24	ABQ81461	Human vascular end
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26	1515.8	98.7	2827	22	AAZ06812	Human LPS, a PDGF-
27	1515.8	98.7	2896	21	AAZ64426	Human platelet-der
28	1515.8	98.7	2898	20	AAZ86352	DNA encoding human
29	1511	98.4	1760	21	AAZ81582	Human zveg3 DNA,
30	1511	98.4	1760	21	AAZ51498	Human growth facto
31	1511	98.4	1760	22	AAZ04649	Human zveg3 DNA
32	1511	98.4	1760	24	ABZ86812	Human CDNA encodin
33	1511	98.4	1760	24	AAZ17443	Human zveg3 codin
34	1511	98.4	1760	25	ABZ93146	DNA encoding human
35	1498.2	97.5	3087	21	AAZ18314	Lung cancer associ
36	1466.4	95.5	2794	21	AAZ48600	Bone morphogenic p
37	1149	74.8	1328	22	AAZ82259	Human VEGF/PDGF-li
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41	956.6	62.3	1134	21	AAA71984	Human VEGF-X DNA f
42	955.6	62.2	1095	21	AAA51540	MBP-ZVEGF3 fusion
43	955.6	62.2	1095	24	ABZ68655	Human zveg3 3/malt
44	955.6	62.2	1095	25	ABZ93189	DNA encoding human
45	953.6	62.1	1134	21	AAA71983	Human VEGF-X DNA f

ALIGNMENTS

RESULT 1

AAA12524
ID AAA12524 standard; CDNA; 1536 BP.

XX AC AAA12524;

XX DT 25-JUL-2000 (first entry)

XX DE CDNA encoding a fragment of platelet-derived growth factor C (PDGF-C).

XX KW Platelet-derived growth factor C; PDGF-C; cell proliferation;

XX KW growth factor; heparin; connective tissue; wound healing; VEGF-P;

XX KW fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;

XX KW choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia;

XX KW lung carcinoma; erythroleukemia; tissue remodelling; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 3..959

XX FT /*tag= a

XX FT /product= "platelet-derived growth factor C fragment"

XX FT /transl_except= (pos: 861...863, aa: Lys)

XX XX WO200018212-A2.

XX XX 06-APR-2000.

XX XX 30-SEP-1999; 99WO-US22668.

XX XX 30-SEP-1998; 98US-0102461.

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QY 1501 AATTAACCTTGTCATCTGATAGGACAGACTGGA 1536

Db 1501 AATTAACCTTGTCATCTGATAGGACAGACTGGA 1536

RESULT 2

AAZ23691

ID AAZ23691 standard; DNA; 2825 BP.

AC AAZ23691;

XX 11-JAN-2000 (first entry)

DT Human VEGF-E DNA.

DE

XX VEGF-E; human; vascular endothelial cell growth factor; wound repair;

KW treatment; cardiovascular disorder; endothelial disorder; therapy;

KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;

KW angiogenic disorder; age-related macular degeneration; vascular disease;

KW neovascularization; tumor; gene mapping; ss.

XX Homo sapiens.

XX

PH Key Location/Qualifiers

FT CDS 259..1296

FT /*tag= a

FT /product= "VEGF-E"

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PN WO9947677-A2.

XX

PD 23-SEP-1999.

XX

PF 10-MAR-1999; 99WO-US05190.

XX

PR 17-MAR-1998; 98US-0040220.

PR 02-NOV-1998; 98US-0184216.

XX

PA (GETH) GENENTECH INC.

XX

PI Ferrara N, Kuo SS;

XX

XX WPI; 1999-580306/49.

DR P-PSDB; AAY33679.

XX

PT New growth factor polypeptide useful for treating cardiovascular or

PT endothelial disorders, e.g. cardiac hypertrophy

XX

PS Claim 2; Fig 1; 122pp; English.

XX

CC This invention describes the isolation of a novel human vascular

CC endothelial cell growth factor-E (VEGF-E) polypeptide which has

CC tranquilizer, vulnery and cardiant activity. VEGF-E can be administered

CC therapeutically, especially by expressing encoding polynucleotides to

CC treat cardiovascular or endothelial disorders in mammals, especially

CC humans. It is useful in wound repair and tissue generation and

CC regeneration, and may especially be used to treat cardiac hypertrophy

CC It can be combined with a carrier in pharmaceutical compositions, which

CC can be administered to treat disorders as above. VEGF-E can be used to

CC screen for antagonists and agonists, and the antagonists administered to

CC treat angiogenic disorders in mammals (especially humans) administered to

CC age-related macular degeneration. It can be used to generate antibodies,

CC useful therapeutically as antagonists, as above. The antibodies are also

CC useful to detect VEGF-E polypeptide, especially to diagnose

CC cardiovascular, endothelial or angiogenic disorders in mammals (e.g.

CC cardiovascular, or neovascularization associated with tumor formation),

CC by contacting the antibody with a tissue sample and detecting formation

CC of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding

CC VEGF-E can be used to diagnose cardiovascular and endothelial disorders

CC in mammals, by detecting abnormally high or low VEGF-E gene expression in

CC tissue samples. They can also be used to diagnose a disease or

CC susceptibility to a disease related to a mutated form of VEGF-E (e.g. a

CC cardiovascular, endothelial or angiogenic disorder such as a tumor), by

CC detecting a mutation in the VEGF-E-encoding sequence isolated from a

CC sample. They may also be used to produce probes useful to detect related

CC sequences or for gene mapping. This sequence encodes the human VEGF-E

XX protein described in the method of the invention.

SQ Sequence 2825 BP; 849 A; 522 C; 605 G; 848 T; 1 other;

Query Match 99.8%; Score 1532.6; DB 20; Length 2825;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTAAATTCAGTTTCCAGCAACAAAGGAAACAGACGAGTACCAAGATCTCTCAGATGAGA 63

Db 341 GTAAATTCAGTTTCCAGCAACAAAGGAAACAGACGAGTACCAAGATCTCTCAGATGAGA 400

QY 64 GAAATTTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGTTTCTCTACTATTATC 123

Db 401 GAAATTTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGTTTCTCTACTATTATC 460

QY 124 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAAC 183

Db 461 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAAC 520

QY 184 TTACGTTTGTATCAAAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGAT 243

Db 521 TTACGTTTGTATCAAAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGAT 580

QY 244 TTGTAGAAGTTTGAGGAACCCAGTGTAGTGAACCTATATTATGGGCGCTGGTGTCTGTA 303

Db 581 TTGTAGAAGTTTGAGGAACCCAGTGTAGTGAACCTATATTATGGGCGCTGGTGTCTGTA 640

QY 304 CTGTACCAAGGAAACAGAGTTTCTAAGGAAATCAATTAGGATAAGATTTGTATCTGATG 363

Db 641 CTGTACCAAGGAAACAGAGTTTCTAAGGAAATCAATTAGGATAAGATTTGTATCTGATG 700

QY 364 AATATTTTCTTCTGAACACAGGGTTCTGCATCCACTACAACATTTGTCATGCCAATTC 423

Db 701 AATATTTTCTTCTGAACACAGGGTTCTGCATCCACTACAACATTTGTCATGCCAATTC 760

QY 424 CAGAAGCTGTGAGTCTTCACTGCTTACCCCTTCACTTTCAGCTTGGCCTGACCTGCTTAATA 483

Db 761 CAGAAGCTGTGAGTCTTCACTGCTTACCCCTTCACTTTCAGCTTGGCCTGACCTGCTTAATA 820

QY 484 ATGCTATAAATGCTCTTGTAGTACCTTGGAGACCTTATTTCGATATCTTGAACACAGAGAT 543

Db 821 ATGCTATAAATGCTCTTGTAGTACCTTGGAGACCTTATTTCGATATCTTGAACACAGAGAT 880

QY 544 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG 603

Db 881 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG 940

QY 604 TTTTGGAGAAATCCAGAGTGTGGATCTGACCTTCACTTTCAGCTTGGCCTGACCTGCTTAATA 663

Db 941 TTTTGGAGAAATCCAGAGTGTGGATCTGAACTTCTTAACTTCAACAGAGAGGTAAATAT 1000

QY 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGAAAGAACTAAGAGAACCGATA 723

Db 1001 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGAAAGAACTAAGAGAACCGATA 1060

QY 724 CCATTTTCTGCCAGGTTGTCTCTCGTTAAACGCTGTGGGGAAGTGTGCTGTTGTC 783

Db 1061 CCATTTTCTGCCAGGTTGTCTCTCGTTAAACGCTGTGGGGAAGTGTGCTGTTGTC 1120

QY 784 TCCCAATTCGAATGAATGTCATGTCTCCCAAGCAAGATTACTAAAAATACCAAGAGG 843

Db 1121 TCCCAATTCGAATGAATGTCATGTCTCCCAAGCAAGATTACTAAAAATACCAAGAGG 1180

QY 844 TCCTTCTAGTTGAGACCAAAACCGGTCTCAGGGGATTTGCACAAATCACTACCCACCGTG 903

Db 1181 TCCTTCTAGTTGAGACCAAAACCGGTCTCAGGGGATTTGCACAAATCACTACCCACCGTG 1240

QY 904 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGTCAGAGGGAGCACAGAGGATAGCCGC 963

Db 1241 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCAGAGGAGTAGCCGC 1300
Qy 964 ATCACCCACGAGCTCTTGGCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAA 1023
Db 1301 ATCACCCACGAGCTCTTGGCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAA 1360
Qy 1024 CGTATGCGTTATCTCCATCTTAATCTCAGTTGTTGCTTCAAGGACCTTTCATCTTCAG 1083
Db 1361 CGTATGCGTTATCTCCATCTTAATCTCAGTTGTTGCTTCAAGGACCTTTCATCTTCAG 1420
Qy 1084 GATTACAGTGCATCTGAAGAGAGAGACATCAACAGAAATTAGAGTTGCAACAGCT 1143
Db 1421 GATTACAGTGCATCTGAAGAGAGAGACATCAACAGAAATTAGAGTTGCAACAGCT 1480
Qy 1144 CTTTTTGAGAGGCGCTTAAAGCAGAGGAGAAAGGTCTTCAATCGTGAAGAAATTA 1203
Db 1481 CTTTTTGAGAGGCGCTTAAAGCAGAGGAGAAAGGTCTTCAATCGTGAAGAAATTA 1540
Qy 1204 ATGTTGTATTAATAGATCACAGCTAGTTTCAAGATTACCATGTACGTATTCCACTAGC 1263
Db 1541 ATGTTGTATTAATAGATCACAGCTAGTTTCAAGATTACCATGTACGTATTCCACTAGC 1600
Qy 1264 TGGGTTCTGTATTCAGTCTTTCGATACGCGCTTAGGCTTAATGTGTCAGTACAGGAAAAA 1323
Db 1601 TGGGTTCTGTATTCAGTCTTTCGATACGCGCTTAGGCTTAATGTGTCAGTACAGGAAAAA 1660
Qy 1324 CTGTGCAAGTGAGCACCTGATTCCGTGCTTGTCTTAATCTTAAAGCTCCATGTCTCTGG 1383
Db 1661 CTGTGCAAGTGAGCACCTGATTCCGTGCTTGTCTTAATCTTAAAGCTCCATGTCTCTGG 1720
Qy 1384 CCTAAATCGTAAATCTGATTTTCTGATACGCGCTTAGGCTTAATGTGTCAGTACATGTA 1443
Db 1721 CCTAAATCGTAAATCTGATTTTCTGATACGCGCTTAGGCTTAATGTGTCAGTACATGTA 1780
Qy 1444 ACCAGACATCTATGTACTACACACCTGCTTTTAAAGAGAACTATGTTGCTATGAAT 1503
Db 1781 ACCAGACATCTATGTACTACACACCTGCTTTTAAAGAGAACTATGTTGCTATGAAT 1840
Qy 1504 TAAACTTGTCATGCTGATGAGCAGACTGGA 1536
Db 1841 TAAACTTGTCATGCTGATGAGCAGACTGGA 1873

RESULT 3
ID ABS57294
AC ABS57294 standard; DNA; 2825 BP.
XX ABS57294;
DI 31-JAN-2003 (first entry)
XX DNA encoding human vascular endothelial cell growth factor-E (VEGF-E).
DE Human; vascular endothelial cell growth factor-E; VEGF-E; PRO:200;
KW VEGF; bone morphogenetic protein 1; wound repair; tissue regeneration;
KW cardiovascular disorder; endothelial disorder; angiogenic disorder;
KW cancer; diabetes mellitus; cardiac hypertrophy; atherosclerosis;
KW cardiast; cytosstatic; antidiabetic; antiarteriosclerotic;
KW gene therapy; gene; ds.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 259..1296
CDS /*tag= a
FT /product= "VEGF-E"
FT
PN US8455283-B1.
XX
XX 24-SEP-2002.
PD
XX 10-MAR-1999; 99US-0265686.
PF

XX 17-MAR-1998; 98US-0040220.
PR 02-NOV-1998; 98US-0184216.
XX (GETH) GENENTECH INC.
PA
XX Ferrara N, Kuo SS;
PI WPI; 2003-066231/06.
XX P-PSDB; ABG72132.
DR
XX New nucleic acid encoding endothelial cell growth factor-E polypeptide,
PT useful for diagnosing or treating a cardiovascular, endothelial or
PT angiogenic disorder such as cancer, diabetes mellitus or
PT atherosclerosis .
XX
XX Claim 2; Fig 1; 46pp; English.
XX
CC The present invention relates to the isolation of human vascular
CC endothelial cell growth factor-E (VEGF-E, also referred to as
CC PRO:200), and the polynucleotide sequence encoding it. VEGF-E is
CC related to VEGF and bone morphogenetic protein 1. VEGF-E is useful
CC in wound repair, as well as in the generation and regeneration of
CC tissue. The sequences of the invention are useful for diagnosing or
CC treating cardiovascular, endothelial or angiogenic disorders such as
CC cancer, diabetes mellitus, cardiac hypertrophy and atherosclerosis.
CC The polynucleotide encoding VEGF-E is useful in the gene therapy of
CC such disorders. The present sequence encodes human VEGF-E.
XX
SQ Sequence 2825 BP; 849 A; 522 C; 605 G; 848 T; 1 other;
Query Match 99.8%; Score 1532.6; DB 25; Length 2825;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 4 GTAAATTCACGTTTCCAGCAACAGGAAACAGAGGAGTACAGATCCTCAGCATGAGA 63
Db 341 GTAAATTCACGTTTCCAGCAACAGGAAACAGAGGAGTACAGATCCTCAGCATGAGA 400
Qy 64 GAAATTTACTGTGTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCTACTATTATC 123
Db 401 GAAATTTACTGTGTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCTACTATTATC 460
Qy 124 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGAAATGTATGATACAAAC 183
Db 461 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGAAATGTATGATACAAAC 520
Qy 184 TTACGTTTGTATGAAAGATTGGGCTTGAAGACCCAGAGAGTACATATGCAAGTATGATT 243
Db 521 TTACGTTTGTATGAAAGATTGGGCTTGAAGACCCAGAGAGTACATATGCAAGTATGATT 580
Qy 244 TTGTAGAAGTTGAGGAACCCAGTGTATGGAACCTATATTAGGCGCTGGTGTCTGGTA 303
Db 581 TTGTAGAAGTTGAGGAACCCAGTGTATGGAACCTATATTAGGCGCTGGTGTCTGGTA 640
Qy 304 CTGTACACAGGAAAAACAGATTTCTAAAGAAATCAAAATTAGGATAAGATTGTATCTGATG 363
Db 641 CTGTACACAGGAAAAACAGATTTCTAAAGAAATCAAAATTAGGATAAGATTGTATCTGATG 700
Qy 364 AATATTTTCTTCTGMAACCGGTTCTGCATCCCACTACAAATGTGTATGCCACATTTCA 423
Db 701 AATATTTTCTTCTGMAACCGGTTCTGCATCCCACTACAAATGTGTATGCCACATTTCA 760
Qy 424 CAGAAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTTCCACTGACCTGCTTAATA 483
Db 761 CAGAAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTTCCACTGACCTGCTTAATA 820
Qy 484 ATGCTATAACCTGCTTTTAGTACCTTTGGAAGACCTTATTCGATATCTTCAACACAGAGAT 543
Db 821 ATGCTATAACCTGCTTTTAGTACCTTTGGAAGACCTTATTCGATATCTTCAACACAGAGAT 880
Qy 544 GGCAGTTGGACTTAGAAGATCTATATAGGCAACTTGTGGCACTTCTTGGCAAGGCTTTTG 603

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Db      881  GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGCTTTTG 940
QY      604  TTTTGGAGAAAAATCCAGAGTGGTGGATCTGAACCTTCTTAAACAGAGGAGGTAAAGATTAT 663
Db      941  TTTTGGAGAAAAATCCAGAGTGGTGGATCTGAACCTTCTTAAACAGAGGAGGTAAAGATTAT 1000
QY      664  ACAGCTGCACACTCGTAACTTCTCAGTGCCTCAATAGGGAAGAACTATAAGAGAACCGATA 723
Db     1001  ACAGCTGCACACTCGTAACTTCTCAGTGCCTCAATAGGGAAGAACTATAAGAGAACCGATA 1060
QY      724  CCATTTTCTGGCCAGGTGTCTCTCGTTAAACGCTGTGTGGCAACTGTGCCCTGTTGTC 783
Db     1061  CCATTTTCTGGCCAGGTGTCTCTCGTTAAACGCTGTGTGGCAACTGTGCCCTGTTGTC 1120
QY      784  TCCACAATGCAATGAATGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACCAAGG 843
Db     1121  TCCACAATGCAATGAATGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACCAAGG 1180
QY      844  TCCTTCAGTTGAGACCAAAACCGGTGTGAGGGGATTCACAAATCACTCACCGACGTGG 903
Db     1181  TCCTTCAGTTGAGACCAAAACCGGTGTGAGGGGATTCACAAATCACTCACCGACGTGG 1240
QY      904  CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGAGCACAGAGGATAGCGC 963
Db     1241  CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGAGCACAGAGGATAGCGC 1300
QY      964  ATCACACAGACGAGCTTGTGCCAGAGCTGTGAGTGCAGTGCAGTGTGATTTATAGAGAA 1023
Db     1301  ATCACACAGACGAGCTTGTGCCAGAGCTGTGAGTGCAGTGCAGTGTGATTTATAGAGAA 1360
QY     1024  CGTATGCGTTATCTCCATCTTAATCTCAGTGTGTTGCTTCAGGACCTTTCATCTTCAG 1083
Db     1361  CGTATGCGTTATCTCCATCTTAATCTCAGTGTGTTGCTTCAGGACCTTTCATCTTCAG 1420
QY     1084  GATTTACAGTGCATTTCTGAAGAGGAGACATCAACAGAAATTAGGAGTTGTGCAACAGCT 1143
Db     1421  GATTTACAGTGCATTTCTGAAGAGGAGACATCAACAGAAATTAGGAGTTGTGCAACAGCT 1480
QY     1144  CTTTTCAGAGGAGGCTTAAGGACAGAGAAAGGTTCTCAATCGTGGAAAGAAATTA 1203
Db     1481  CTTTTCAGAGGAGGCTTAAGGACAGAGAAAGGTTCTCAATCGTGGAAAGAAATTA 1540
QY     1204  ATGTTGTATTAAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGTATTCCTAGC 1263
Db     1541  ATGTTGTATTAAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGTATTCCTAGC 1600
QY     1264  TGGGTTCTGTATTTCAAGTCTTTTCGATACGGCTTAGGGTAATGTCAATCGTGGAAAAA 1323
Db     1601  TGGGTTCTGTATTTCAAGTCTTTTCGATACGGCTTAGGGTAATGTCAATCGTGGAAAAA 1660
QY     1324  CTGTGCAAGTGAGCACCTGATTCGGTTCCTTCGTTAACTCTAAAGCTCCATGCTCTGG 1383
Db     1661  CTGTGCAAGTGAGCACCTGATTCGGTTCCTTCGTTAACTCTAAAGCTCCATGCTCTGG 1720
QY     1384  CCTAAATCGTATATAAATCTGAAATTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATG 1443
Db     1721  CCTAAATCGTATATAAATCTGAAATTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATG 1780
QY     1444  ACCAGAACATTTATGTACTACAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGAAT 1503
Db     1781  ACCAGAACATTTATGTACTACAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGAAT 1840
QY     1504  TAAACTGTGTCTATGCTGTAGACAGACTGGA 1536
Db     1841  TAAACTGTGTCTATGCTGTAGACAGACTGGA 1873
```

RESULT 4

AAZ34296

ID AAZ34296 standard; cDNA; 2849 BP.

XX

AC

AAZ34296;

XX

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DT      07-DEC-1999 (first entry)
XX      Human PR0200 nucleotide sequence.
XX      Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
XX      probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX      secreted protein; transmembrane protein; ss.
XX      Homo sapiens.
XX      WO9946281-A2.
XX      16-SEP-1999.
XX      08-MAR-1999; 99WO-US05028.
XX      10-MAR-1998; 98US-0077450.
XX      11-MAR-1998; 98US-0077632.
XX      11-MAR-1998; 98US-0077641.
XX      11-MAR-1998; 98US-0077649.
XX      12-MAR-1998; 98US-0077791.
XX      13-MAR-1998; 98US-0078004.
XX      17-MAR-1998; 98US-0040220.
XX      20-MAR-1998; 98US-0078886.
XX      20-MAR-1998; 98US-0078910.
XX      20-MAR-1998; 98US-0078936.
XX      20-MAR-1998; 98US-0078939.
XX      25-MAR-1998; 98US-0079294.
XX      26-MAR-1998; 98US-0079656.
XX      27-MAR-1998; 98US-0079663.
XX      27-MAR-1998; 98US-0079664.
XX      27-MAR-1998; 98US-0079689.
XX      27-MAR-1998; 98US-0079728.
XX      27-MAR-1998; 98US-0079786.
XX      30-MAR-1998; 98US-0079920.
XX      30-MAR-1998; 98US-0079923.
XX      31-MAR-1998; 98US-0080105.
XX      31-MAR-1998; 98US-0080107.
XX      31-MAR-1998; 98US-0080165.
XX      31-MAR-1998; 98US-0080194.
XX      01-APR-1998; 98US-0080327.
XX      01-APR-1998; 98US-0080328.
XX      01-APR-1998; 98US-0080333.
XX      01-APR-1998; 98US-0080334.
XX      08-APR-1998; 98US-0081049.
XX      08-APR-1998; 98US-0081070.
XX      08-APR-1998; 98US-0081071.
XX      09-APR-1998; 98US-0081195.
XX      09-APR-1998; 98US-0081203.
XX      09-APR-1998; 98US-0081229.
XX      15-APR-1998; 98US-0081817.
XX      15-APR-1998; 98US-0081838.
XX      15-APR-1998; 98US-0081952.
XX      15-APR-1998; 98US-0081955.
XX      21-APR-1998; 98US-0082568.
XX      21-APR-1998; 98US-0082569.
XX      22-APR-1998; 98US-0082700.
XX      22-APR-1998; 98US-0082704.
XX      23-APR-1998; 98US-0082804.
XX      23-APR-1998; 98US-0082767.
XX      23-APR-1998; 98US-0082796.
XX      27-APR-1998; 98US-0083336.
XX      28-APR-1998; 98US-0083322.
XX      29-APR-1998; 98US-0083392.
XX      29-APR-1998; 98US-0083495.
XX      29-APR-1998; 98US-0083496.
XX      29-APR-1998; 98US-0083499.
XX      29-APR-1998; 98US-0083500.
XX      29-APR-1998; 98US-0083545.
XX      29-APR-1998; 98US-0083554.
XX      29-APR-1998; 98US-0083558.
XX      29-APR-1998; 98US-0083559.
XX      30-APR-1998; 98US-0083742.
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QY 124 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATGTATGGATACAAAC 183
Db 487 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATGTATGGATACAAAC 546
QY 184 TTACGTTTGATGAAAGATTGGGCTTGAGACCCAGAGATGACATATGCAAGTATGATT 243
Db 547 TTACGTTTGATGAAAGATTGGGCTTGAGACCCAGAGATGACATATGCAAGTATGATT 606
QY 244 TTGTAGAAAGTTGAGAAACCCAGTGTATGAACTATATTAGGGCGCTGGTGTCTCGGTA 303
Db 607 TTGTAGAAAGTTGAGAAACCCAGTGTATGAACTATATTAGGGCGCTGGTGTCTCGGTA 666
QY 304 CTGTACCAAGGAAAAAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 363
Db 667 CTGTACCAAGGAAAAAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 726
QY 364 AATATTTTCCCTTCGAACACAGGTTCTGCATCCACTACAACTTCTCATGCCACAATTCA 423
Db 727 AATATTTTCCCTTCGAACACAGGTTCTGCATCCACTACAACTTCTCATGCCACAATTCA 786
QY 424 CAGAAGCTGTGAGTCCCTTCAGTGTACCCCTTTCAGCTTTGCCACTGGACCTGCTTAATA 483
Db 787 CAGAAGCTGTGAGTCCCTTCAGTGTACCCCTTTCAGCTTTGCCACTGGACCTGCTTAATA 846
QY 484 ATGCTATAACTGCCCTTTAGTACCTTGGGAAGACCTTATTTCGATATCTTGAAACAGAGAT 543
Db 847 ATGCTATAACTGCCCTTTAGTACCTTGGGAAGACCTTATTTCGATATCTTGAAACAGAGAT 906
QY 544 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAGGCTTTTG 603
Db 907 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAGGCTTTTG 966
QY 604 TTTTGGGAAGAAATCCAGAGTGTGGATCTGAACCTTCTAACAGAGAGGTAAAGATTAT 663
Db 967 TTTTGGGAAGAAATCCAGAGTGTGGATCTGAACCTTCTAACAGAGAGGTAAAGATTAT 1026
QY 664 ACAGTGCACACTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGGAACCGATA 723
Db 1027 ACAGTGCACACTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGGAACCGATA 1086
QY 724 CCATTTCTGCCAGGTTGTCTCCTGGTTAAACGCTGTGGGAACCTGCTCGCTTTTC 783
Db 1087 CCATTTCTGCCAGGTTGTCTCCTGGTTAAACGCTGTGGGAACCTGCTCGCTTTTC 1146
QY 784 TCCAAATTCGAATGAATGTCAAATGTGTCCCAAGCAAAAGTTTACTAAAAAATACCACGAGG 843
Db 1147 TCCAAATTCGAATGAATGTCAAATGTGTCCCAAGCAAAAGTTTACTAAAAAATACCACGAGG 1206
QY 844 TCCTTCAGTTGAGACCAAAACCGGTGTGAGGGGATTCGCAAAATCACTCACCGACGTGG 903
Db 1207 TCCTTCAGTTGAGACCAAAACCGGTGTGAGGGGATTCGCAAAATCACTCACCGACGTGG 1266
QY 904 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGCGAGGGGAGCACAGAGGATAGCCGC 963
Db 1267 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGCGAGGGGAGCACAGAGGATAGCCGC 1326
QY 964 ATCACCAACAGAGCTTTGCCCAGAGCTGTGCAAGTGCAGTGGCTGATTCTATTAGAGAA 1023
Db 1327 ATCACCAACAGAGCTTTGCCCAGAGCTGTGCAAGTGCAGTGGCTGATTCTATTAGAGAA 1386
QY 1024 CGTATCGGTTATCTCCATCCCTTAATCTCAGTTGTTGCTTCAAGAACCTTTCATCTTCAAG 1083
Db 1387 CGTATCGGTTATCTCCATCCCTTAATCTCAGTTGTTGCTTCAAGAACCTTTCATCTTCAAG 1446
QY 1084 GATTATCAGTGCATTTCTGAAAAGAGAGACATCAAAACAGAAATTTAGGAGTTGCAACAGCT 1143
Db 1447 GATTATCAGTGCATTTCTGAAAAGAGAGACATCAAAACAGAAATTTAGGAGTTGCAACAGCT 1506
QY 1144 CTTTGTGAGAGAGGCTTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAAGAAATTA 1203
Db 1507 CTTTGTGAGAGAGGCTTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAAGAAATTA 1566
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QY 1204 ATGTTGTATTAAATAGATCACCCAGCTAGTTTCAGAGTTACCAATGATCGTATTCCTAGC 1263
Db 1567 ATGTTGTATTAAATAGATCACCCAGCTAGTTTCAGAGTTACCAATGATCGTATTCCTAGC 1626
QY 1264 TGGGTTCTGTATTTCAGTTCCTTTCATACGGCTTAGGGTAAATGTCAGTACGGAAGAAA 1323
Db 1627 TGGGTTCTGTATTTCAGTTCCTTTCATACGGCTTAGGGTAAATGTCAGTACGGAAGAAA 1686
QY 1324 CTGTGCAAGTGAGCACCTGATTCCTTGCCTTAACTCTAAAGCTCCATGTCCTGGG 1383
Db 1687 CTGTGCAAGTGAGCACCTGATTCCTTGCCTTAACTCTAAAGCTCCATGTCCTGGG 1746
QY 1384 CCTAAAAATCGTATAAAAAATCTCGATTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTA 1443
Db 1747 CCTAAAAATCGTATAAAAAATCTCGATTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTA 1806
QY 1444 ACCGAACATTTCTATGTACTACAACTGGTTTTTTTTTTTTTTTTTTTAAAGGAATATGTTCTATGA 1503
Db 1807 ACCGAACATTTCTATGTACTACAACTGGTTTTTTTTTTTTTTTTTTTAAAGGAATATGTTCTATGA 1866
QY 1504 TAAACTTGTGCATCTGCTGATAGGACAGACTGGA 1536
Db 1867 TAAACTTGTGCATCTGCTGATAGGACAGACTGGA 1899

RESULT 7
AAC58579
ID AAC58579 standard; cDNA; 2849 BP.
XX
AC AAC58579;
XX
DT 29-JAN-2001 (first entry)
DE Human PRO200 protein UNQ174 encoding cDNA SEQ ID NO:1.
XX
KW Human; immune related disease; diagnosis; Sjogren's syndrome; antiinflammatory; cardiant; dermatological; antihypertensive; antirheumatic; immunosuppressive; haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective; antianemic; hepatotropic; virucide; antipsoriatic; antiallergic; antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopenia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; immunological disease; transplantation associated disease; graft rejection; graft-versus-host-disease; ss.
XX
OS Homo sapiens.
XX
PN WO200053758-A2.
XX
PD 14-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US05841.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99US-0123618.
PR 12-MAR-1999; 99US-0123957.
PR 12-APR-1999; 99US-0125775.
PR 20-APR-1999; 99US-0128849.
PR 28-APR-1999; 99WO-US08615.
PR 04-MAY-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0132371.
PR 02-JUN-1999; 99US-0134287.
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99WO-US20111.
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PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 15-SEP-1999; 99WO-US22089.
 PR 29-OCT-1999; 99US-0162506.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
 XX
 DR WPI; 2000-572271/53.
 DR P-PSDB; AAB33414.
 XX
 PT sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
 XX
 PS Claim 23; Fig 1; 309pp; English.
 XX
 CC The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
 CC autoimmune or immune-mediated skin diseases, allergic diseases,
 CC immunological diseases of the lung, and transplantation associated
 CC diseases including graft rejection and graft-versus-host-disease.
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Query Match 99.8%; Score 1532.6; DB 21; Length 2849;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GTAATATCCAGTTTCCGACACAGGACAGACGAGTACAGATCTCTAGCATGAGA 63
 DB 367 GTAATATCCAGTTTCCGACACAGGACAGACGAGTACAGATCTCTAGCATGAGA 426
 QY 64 GAAATATTACTGTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCTACTATTTC 123
 DB 427 GAAATATTACTGTCTACTAATGGAAGTATTACAGCCCAAGGTTTCTCTACTATTTC 486

QY 124 CAAGAAATACGGTCTTGGTATCGAGATTAGTAGCAGTAGAGAAAATGTATGATCAAC 183
 DB 487 CAAGAAATACGGTCTTGGTATCGAGATTAGTAGCAGTAGAGAAAATGTATGATCAAC 546
 QY 184 TTACGTTTGATCAAGATTGTTGGCTTGAAGACCCGAGAGATGACATATGCAAGTAGTATT 243
 DB 547 TTACGTTTGATCAAGATTGTTGGCTTGAAGACCCGAGAGATGACATATGCAAGTAGTATT 606
 QY 244 TTGTAGAGTTGAGGAACCCAGTGATGGAACCTATATTAGGGCGCTGGTGGTCTGGTA 303
 DB 607 TTGTAGAGTTGAGGAACCCAGTGATGGAACCTATATTAGGGCGCTGGTGGTCTGGTA 666
 QY 304 CTGTATACAGAAAACAGATTTCTTAAGGAAATCAAAATTAGGATAGATTTGTATCTGATG 363
 DB 667 CTGTATACAGAAAACAGATTTCTTAAGGAAATCAAAATTAGGATAGATTTGTATCTGATG 726
 QY 364 AATATTTTCCTTCTGAACAGGGTCTGCATCCATCAACAAATTGTCATGCCACAATTCA 423
 DB 727 AATATTTTCCTTCTGAACAGGGTCTGCATCCATCAACAAATTGTCATGCCACAATTCA 786
 QY 424 CAGAAGCTGTGAGTCTTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATA 483
 DB 787 CAGAAGCTGTGAGTCTTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATA 846
 QY 484 ATGCTATAACCTGCTTTAGTACCTTGGAGACCTTATTCGATATCTTTGAACACAGAGAT 543
 DB 847 ATGCTATAACCTGCTTTAGTACCTTGGAGACCTTATTCGATATCTTTGAACACAGAGAT 906
 QY 544 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGCTTTTG 603
 DB 907 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGCTTTTG 966
 QY 604 TTTTGGAGAAATCCAGAGTGGTGAATCTGAACCTTCTTAACAGAGGAGTAAGATTAT 663
 DB 967 TTTTGGAGAAATCCAGAGTGGTGAATCTGAACCTTCTTAACAGAGGAGTAAGATTAT 1026
 QY 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTTAAAGAGAACCGATA 723
 DB 1027 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTTAAAGAGAACCGATA 1086
 QY 724 CCAATTTCTGGCAGGTTGTCTCTGGTTAAACGCTGTGTGGGAACTGTGCTGCTTTGTC 783
 DB 1087 CCAATTTCTGGCAGGTTGTCTCTGGTTAAACGCTGTGTGGGAACTGTGCTGCTTTGTC 1146
 QY 784 TCCCAATTTGCAATCAATGTCAATGTCTCCCAAGCAAGTACTTAAATAATCCAGAGG 843
 DB 1147 TCCCAATTTGCAATCAATGTCAATGTCTCCCAAGCAAGTACTTAAATAATCCAGAGG 1206
 QY 844 TCCTTCAGTTGAGACCAASACCGGTGTCCAGGGATTGCACAAATCACTCACCGAGTGG 903
 DB 1207 TCCTTCAGTTGAGACCAASACCGGTGTCCAGGGATTGCACAAATCACTCACCGAGTGG 1266
 QY 904 CCCTGGAGCACCATGAGAGTGTGATGTGTGTCAGAGGGAGCAGAGAGATAGCCGC 963
 DB 1267 CCCTGGAGCACCATGAGAGTGTGATGTGTGTCAGAGGGAGCAGAGAGATAGCCGC 1326
 QY 964 ATCACACACAGCAGCTCTTTGCCAGAGCTGTGACGTGCGTGTGATTTCTATTAGAGAA 1023
 DB 1327 ATCACACACAGCAGCTCTTTGCCAGAGCTGTGACGTGCGTGTGATTTCTATTAGAGAA 1386
 QY 1024 CGTATGCGTTATCTCCATCTTAATCTCAGTTGTTGTTTCAAGGACCTTTTCATCTTCAG 1083
 DB 1387 CGTATGCGTTATCTCCATCTTAATCTCAGTTGTTGTTTCAAGGACCTTTTCATCTTCAG 1446
 QY 1084 GATTATACGTGATCTGAAAGAGAGACATCAAAAGATTTAGAGTTGTGCAACAGCT 1143
 DB 1447 GATTATACGTGATCTGAAAGAGAGACATCAAAAGATTTAGAGTTGTGCAACAGCT 1506
 QY 1144 CTTTTGAGAGAGGCTTAAAGACAGGAGAAAAGTCTTCAATCGTGAAGAAAATTA 1203
 DB 1507 CTTTTGAGAGAGGCTTAAAGACAGGAGAAAAGTCTTCAATCGTGAAGAAAATTA 1566


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Qy 664 ACAGTTCGACACCTCGTAACCTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCCGATA 723
Db 1027 ACAGCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCCGATA 1086
Qy 724 CCATTTTCTGCGCAGGTTGCTCTCTGTTTAAACGCTGTGTGGAACTGTGCGCTTGTGTC 783
Db 1087 CCATTTTCTGCGCAGGTTGCTCTCTGTTTAAACGCTGTGTGGAACTGTGCGCTTGTGTC 1146
Qy 784 TCCACAAATTCGAATGAATGTCATGTCCTCCAAAGCAAGTTACTAAAAATACCAACGAGG 843
Db 1147 TCCACAAATTCGAATGAATGTCATGTCCTCCAAAGCAAGTTACTAAAAATACCAACGAGG 1206
Qy 844 TCCCTTCAGTTGAGACCAAAACCGGTGTGAGGGGATTCGCAAAATCACTACCCAGCGTGG 903
Db 1207 TCCCTTCAGTTGAGACCAAAACCGGTGTGAGGGGATTCGCAAAATCACTACCCAGCGTGG 1266
Qy 904 CCCTGGAGCACCATGAGAGGTGACGTGTGTGTCAGAGGGAGCAGAGGATAGCCGC 963
Db 1267 CCCTGGAGCACCATGAGAGGTGACGTGTGTGTCAGAGGGAGCAGAGGATAGCCGC 1326
Qy 964 ATCACCACGACGCTCTTGCCACAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAA 1023
Db 1327 ATCACCACGACGCTCTTGCCACAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAA 1386
Qy 1024 CGTATGCGTTATCTCCATCTTAATCTCAGTTGTTTGCCTCAAGGACCTTTTCATCTTCAG 1083
Db 1387 CGTATGCGTTATCTCCATCTTAATCTCAGTTGTTTGCCTCAAGGACCTTTTCATCTTCAG 1446
Qy 1084 GATTTACAGTGCAATCTGAAGAGGAGACATCAACAGAAATAGAGTGTGCAACAGCT 1143
Db 1447 GATTTACAGTGCAATCTGAAGAGGAGACATCAACAGAAATAGAGTGTGCAACAGCT 1506
Qy 1144 CTTTTGAGAGGAGCCCTAAAGACAGGAGAAAGTCTTCAATCGTGAAGAAATTA 1203
Db 1507 CTTTTGAGAGGAGCCCTAAAGACAGGAGAAAGTCTTCAATCGTGAAGAAATTA 1566
Qy 1204 ATGTTGTATTAATAGATACACAGCTAGTTTTCAGAGTTACCATGTAGTATTCACATAGC 1263
Db 1567 ATGTTGTATTAATAGATACACAGCTAGTTTTCAGAGTTACCATGTAGTATTCACATAGC 1626
Qy 1264 TGGGTTCTGTATTTTCAGTTCTTTTGCATACGCTTAGGTATGTACGTACAGGAAAAA 1323
Db 1627 TGGGTTCTGTATTTTCAGTTCTTTTGCATACGCTTAGGTATGTACGTACAGGAAAAA 1686
Qy 1324 CTGTGCAAGTGAGACACCTGATTCGCTTGCTTAACTCTAAAGCTCCCATGTCCTGGG 1383
Db 1687 CTGTGCAAGTGAGACACCTGATTCGCTTGCTTAACTCTAAAGCTCCCATGTCCTGGG 1746
Qy 1384 CCTAAATCGTATATAAATCTGGATTTTTTTTTTTTTTTTTTTTGTGCTCATATTCATATGTAA 1443
Db 1747 CCTAAATCGTATATAAATCTGGATTTTTTTTTTTTTTTTTTTTGTGCTCATATTCATATGTAA 1806
Qy 1444 ACCAGACATTTCTATGTACTACAAACCTGGTTTTTAAAGAGAACTATGTTGCTATGAAT 1503
Db 1807 ACCAGACATTTCTATGTACTACAAACCTGGTTTTTAAAGAGAACTATGTTGCTATGAAT 1866
Qy 1504 TAAACTTGTGTCTAGCTGTATAGGACAGACTGGA 1536
Db 1867 TAAACTTGTGTCTAGCTGTATAGGACAGACTGGA 1899
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RESULT 9

AAS21386

ID AAS21386 standard; cDNA; 2849 BP.

XX AC AAS21386;

XX AC AAS21386;

XX 24-OCT-2001 (first entry)

XX Human cDNA sequence encoding for PRO200 polypeptide.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;

breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.

Homo sapiens.

WO200140466-A2.

07-JUN-2001.

01-DEC-2000; 2000WO-US32678.

01-DEC-1999; 99WO-US28301.

01-DEC-1999; 99WO-US28634.

02-DEC-1999; 99WO-US28551.

02-DEC-1999; 99WO-US28564.

02-DEC-1999; 99WO-US28565.

09-DEC-1999; 99US-0170282.

16-DEC-1999; 99WO-US30911.

20-DEC-1999; 99WO-US30999.

30-DEC-1999; 99WO-US31243.

06-JAN-2000; 2000WO-US00277.

06-JAN-2000; 2000WO-US00376.

11-FEB-2000; 2000WO-US03565.

18-FEB-2000; 2000WO-US04341.

18-FEB-2000; 2000WO-US04342.

22-FEB-2000; 2000WO-US04414.

24-FEB-2000; 2000WO-US04914.

24-FEB-2000; 2000WO-US05004.

01-MAR-2000; 2000WO-US05601.

21-MAR-2000; 2000WO-US07377.

30-MAR-2000; 2000WO-US07532.

17-MAY-2000; 2000WO-US13705.

22-MAY-2000; 2000WO-US14042.

30-MAY-2000; 2000WO-US14941.

02-JUN-2000; 2000WO-US15264.

10-NOV-2000; 2000WO-US30873.

(GETH) GENENTECH INC.

Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;

Gerritsen ME, Goddard A, Godowski PJ, Gurney AT, Sherwood S;

Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2001-408281/43.

P-FSDB; AAU12314.

Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical -

Claim 3; Fig 285; 813pp; English.

AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify

CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Query Match 99.8%; Score 1532.6; DB 22; Length 2849;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	4	GTAAATCCAGTTTCCAGCAACAGGAACAGAGTACAGATCCTCAGCATGAGA	63
DB	367	GTAAATCCAGTTTCCAGCAACAGGAACAGAGTACAGATCCTCAGCATGAGA	426
QY	64	GAATATTACTGTCTACTAATGGAAGTATTCACAGCCCAAGTTTCTCATCTATC	123
DB	427	GAATATTACTGTCTACTAATGGAAGTATTCACAGCCCAAGTTTCTCATCTATC	486
QY	124	CAAGAAATACGCTCTTGGTATGAGATTAGTAGCAGTAGAGGAATATGATGATACAC	183
DB	487	CAAGAAATACGCTCTTGGTATGAGATTAGTAGCAGTAGAGGAATATGATGATACAC	546
QY	184	TTACGTTTGTAAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT	243
DB	547	TTACGTTTGTAAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT	606
QY	244	TGTGTAAGTTGAGAAACCAAGTATGGAATATATTAGGCGCTGGTGTCTCGGTA	303
DB	607	TGTGTAAGTTGAGAAACCAAGTATGGAATATATTAGGCGCTGGTGTCTCGGTA	666
QY	304	CTGTACACAGGAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTGATCTGATG	363
DB	667	CTGTACACAGGAAACAGATTTCTAAAGGAAATCAAAATTAGGATAAGATTGATCTGATG	726
QY	364	AATATTTTCTTGAACACAGGTTCTGCATCCACTACAAATTTGTCATGCCAATTCAC	423
DB	727	AATATTTTCTTGAACACAGGTTCTGCATCCACTACAAATTTGTCATGCCAATTCAC	786
QY	424	CAGAGCTGTGAGTCTTCAAGTCTACCCCTTCAAGTCTGAGTCTGAGCTGCTTAATA	483
DB	787	CAGAGCTGTGAGTCTTCAAGTCTACCCCTTCAAGTCTGAGTCTGAGCTGCTTAATA	846
QY	484	ATGCTATAACGCTTTAGTACCTTGGAGACCTTATTCGATATCTTGAACACAGAGAT	543
DB	847	ATGCTATAACGCTTTAGTACCTTGGAGACCTTATTCGATATCTTGAACACAGAGAT	906
QY	544	GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTG	603
DB	907	GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTG	966
QY	604	TTTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTACAGAGAGGTAAATAT	663
DB	967	TTTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTACAGAGAGGTAAATAT	1026
QY	664	ACAGCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAAGAACTTAAAGAGAACCGATA	723
DB	1027	ACAGCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAAGAACTTAAAGAGAACCGATA	1086
QY	724	CAATTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTGTGGGAACCTGTGCTGTGTC	783
DB	1087	CAATTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTGTGGGAACCTGTGCTGTGTC	1146
QY	784	TCCCAATTTGCAATGCAATGCTATGCTCCAGCAAAAGTACTAAAAATACCAAGAGG	843
DB	1147	TCCCAATTTGCAATGCAATGCTATGCTCCAGCAAAAGTACTAAAAATACCAAGAGG	1206
QY	844	TCCTTCAGTTGAGACAAASACCGGTGTGAGGGGATTCACAAATCACTCACCGACGTGG	903
DB	1207	TCCTTCAGTTGAGACAAASACCGGTGTGAGGGGATTCACAAATCACTCACCGACGTGG	1266
QY	904	CCCTGGAGCAACATGAGAGTGTGATGTGTGTGAGAGGGAGCACAGGAGGATAGCCGC	963
DB	1267	CCCTGGAGCAACATGAGAGTGTGATGTGTGTGAGAGGGAGCACAGGAGGATAGCCGC	1326

QY	964	ATCACACACAGCAGCTTTGCCACAGAGCTGTGCAGTGCAGTGGCTGATTTCTATTAGAGAA	1023
DB	1327	ATCACACACAGCAGCTTTGCCACAGAGCTGTGCAGTGCAGTGGCTGATTTCTATTAGAGAA	1386
QY	1024	CGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGGCTTCAAGACCTTTCATCTTCAG	1083
DB	1387	CGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGGCTTCAAGACCTTTCATCTTCAG	1446
QY	1084	GAATTTACAGTGCATTTCTGAAGAGAGACATCAACAGAAATAGGAGTTGTGCAACAGCT	1143
DB	1447	GAATTTACAGTGCATTTCTGAAGAGAGACATCAACAGAAATAGGAGTTGTGCAACAGCT	1506
QY	1144	CTTTTGAAGAGGCGCTAAAGACAGGAGAAAAGTCTTCAATCTGTGGAAGAAAATTA	1203
DB	1507	CTTTTGAAGAGGCGCTAAAGACAGGAGAAAAGTCTTCAATCTGTGGAAGAAAATTA	1566
QY	1204	ATGTTGTATTAATAGATCACCAGCTAGTTTCAGAGTTTACCATTGTACGTATTTCCACTAGC	1263
DB	1567	ATGTTGTATTAATAGATCACCAGCTAGTTTCAGAGTTTACCATTGTACGTATTTCCACTAGC	1626
QY	1264	TGGGTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAA	1323
DB	1627	TGGGTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAA	1586
QY	1324	CTGTGCAAGTGAAGCCTGATTCCTGTTGCTTAACTCTAAAGCTCCATGTCTCTGGG	1383
DB	1687	CTGTGCAAGTGAAGCCTGATTCCTGTTGCTTAACTCTAAAGCTCCATGTCTCTGGG	1746
QY	1384	CCTAAATCGTATAAATCTGGAATTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTA	1443
DB	1747	CCTAAATCGTATAAATCTGGAATTTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTA	1806
QY	1444	ACCAGACATTTCTATGTACTACAAACCTGGTTTAAAAAGGAACTATGTGTCTATGAAT	1503
DB	1807	ACCAGACATTTCTATGTACTACAAACCTGGTTTAAAAAGGAACTATGTGTCTATGAAT	1866
QY	1504	TAAACTGTGTCTGCTGATAGGACAGACTGGA	1536
DB	1867	TAAACTGTGTCTGCTGATAGGACAGACTGGA	1899

RESULT 10

AAC90564

ID AAC90564 standard; cDNA; 2849 BP.

XX AAC90564;

XX AC

DT 21-MAR-2001 (first entry)

XX Human PRO200 cDNA.

DE Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;

KW vasotropic; antiarthritic; antiarthritic; antiinflammatory; cytostatic;

KW vulnery; antiangular; gene therapy; cardiovascular disease;

KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;

KW wound healing; ss.

OS Homo sapiens.

XX WO200073445-A2.

FN 07-DEC-2000.

XX 17-MAY-2000; 2000WO-US13705.

XX 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

 PR 20-JUL-1999; 99US-0144758. || PR 26-JUL-1999; 99US-0145698. | |
PR 28-JUL-1999; 99US-0146222.	
PR 01-SEP-1999; 99WO-US20111.	
PR 30-NOV-1999; 99WO-US28313.	

Db	787	CAGAGCTGTGAGTCTCTTCAGTGTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATA	846	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
QY	484	ATGCTATTAACCTGCTTTAGTACCTTGGAGACCTTATTTCGATATCTTGAACCCAGAGAT	543	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
Db	847	ATGCTATTAACCTGCTTTAGTACCTTGGAGACCTTATTTCGATATCTTGAACCCAGAGAT	906	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
QY	544	GCGAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG	603	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
Db	907	GCGAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG	966	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
QY	604	TTTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGAGGTAAAGATTAT	663	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
Db	967	TTTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGAGGTAAAGATTAT	1026	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
QY	664	ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTTAAAGAGAACCGATA	723	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
Db	1027	ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTTAAAGAGAACCGATA	1086	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
QY	724	CCATTTTCTGGCCAGGTTGTCTCTGTTTAAACCGCTGTGGTGGAACTGTGCTGTGTC	783	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
Db	1087	CCATTTTCTGGCCAGGTTGTCTCTGTTTAAACCGCTGTGGTGGAACTGTGCTGTGTC	1146	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
QY	784	TCCCAATTTGCATGAATGTCAATGTGTCCGAGCAAAAGTTACTTAAAAATACCAAGAGG	843	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
Db	1147	TCCCAATTTGCATGAATGTCAATGTGTCCGAGCAAAAGTTACTTAAAAATACCAAGAGG	1206	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
QY	844	TCCTTCAGTTGAGACCAAAACCCGCTGTCCAGGGGATTGCACAAATCACTCACCGACGTGG	903	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
Db	1207	TCCTTCAGTTGAGACCAAAACCCGCTGTCCAGGGGATTGCACAAATCACTCACCGACGTGG	1266	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
QY	904	CCCTGGAGCACCATGAGGAGTGTGCTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGC	963	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
Db	1267	CCCTGGAGCACCATGAGGAGTGTGCTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGC	1326	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
QY	964	ATCACCAACAGCAGCTCTTCCACAGCTGTCCAGTGCAGTGCAGTGCATCTATTAGAGAA	1023	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
Db	1327	ATCACCAACAGCAGCTCTTCCACAGCTGTCCAGTGCAGTGCAGTGCATCTATTAGAGAA	1386	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
QY	1024	CGTATGCTTATCTCCATCTTAACTCTCAGTTGTTTGTCTCAAGGACCTTTCATCTTCAAG	1083	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
Db	1387	CGTATGCTTATCTCCATCTTAACTCTCAGTTGTTTGTCTCAAGGACCTTTCATCTTCAAG	1446	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
QY	1084	GATTTCAGTGCATCTGAAAGAGAGACATCAAAACAGAAATPAGAGTTGTGCAACAGCT	1143	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
Db	1447	GATTTCAGTGCATCTGAAAGAGAGACATCAAAACAGAAATPAGAGTTGTGCAACAGCT	1506	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
QY	1144	CTTTTGGAGAGGGCTTAAAGACAGGAGAAAGCTTTCATCTGCGGAAAGAAATTTAA	1203	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
Db	1507	CTTTTGGAGAGGGCTTAAAGACAGGAGAAAGCTTTCATCTGCGGAAAGAAATTTAA	1566	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
QY	1204	ATGTTGTATTAATAGATCACAGCTAGTTTCCAGAGTTACCATGTACGTATTTCCACTAGC	1263	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
Db	1567	ATGTTGTATTAATAGATCACAGCTAGTTTCCAGAGTTACCATGTACGTATTTCCACTAGC	1626	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
QY	1264	TGGTTTCTGATTTTCAGTCTTTTCATACGCTTGGTATAGTGCAGTACAGAGAAAAAA	1323	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
Db	1627	TGGTTTCTGATTTTCAGTCTTTTCATACGCTTGGTATAGTGCAGTACAGAGAAAAAA	1686	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
QY	1324	CTGTGCAAGTGCAGCCTGATTTCCGTTGCTTTCATCTTAAAGCTCCATGCTCTGGG	1383	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
Db	1687	CTGTGCAAGTGCAGCCTGATTTCCGTTGCTTTCATCTTAAAGCTCCATGCTCTGGG	1746	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
QY	1384	CCTAAAATCGTATAAAATCTGGAATTTTTTTTTTTTTTTTGTCTCATATTCATATGTAA	1443	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
Db	1747	CCTAAAATCGTATAAAATCTGGAATTTTTTTTTTTTTTTTGTCTCATATTCATATGTAA	1806	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
QY	1444	ACCAGAACTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT	1503	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
Db	1807	ACCAGAACTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT	1866	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899
QY	1504	TAACTTCTGTCATGCTGATAGGACAGACTGGA	1536	Db	1867	TAAACTTGTGTCATGCTGATAGGACAGACTGGA	1899

RESULT 13
ID ACA03745 standard; cDNA; 2849 BP.
AC ACA03745;
XX
DT 23-MAY-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #143.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder;
KW cytoskeletal; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003036180-A1.
XX
PD 20-FEB-2003.
XX
PF 09-MAY-2002; 2002US-0143114.
XX
PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US22089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
PR (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff B, Gao W;
PI Gerritsen ME, Goddard A, Godowski PU, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-332040/31.
DR P-PSDB; ABU66712.
XX
PT New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in
PT tissue typing, and in chromosome identification -
XX
PS Claim 2; Fig 285; 660pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,

CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for identifying agonists or antagonists.
CC The PRO polypeptides are useful for stimulating the release of
CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating
CC the proliferation or differentiation of chondrocytes, and detecting the
CC presence of tumours. The polynucleotide sequences encoding PRO
CC polypeptides are useful as hybridisation probes, in chromosome and
CC gene mapping, in the generation of antisense RNA and DNA, in the
CC preparation of PRO polypeptides, for generating transgenic animals or
CC knockout animals, for the genetic analysis of individuals with genetic
CC disorders, and in gene therapy. AC03603-ACA03877 represent cDNAs
CC encoding the human PRO polypeptides of the invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsIDEntry.html.
XX
SQ Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;
Query Match 99.8%; Score 1532.6; DB 25; Length 2849;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 GTAAATCCAGTTTCCAGCAACAGGACAGAAACGAGTCAAGATCCTCAGCATGAGA 63
DB 367 GTAAATCCAGTTTCCAGCAACAGGACAGAAACGAGTCAAGATCCTCAGCATGAGA 426
QY 64 GAATATTACTGTGTCTACTAATGAAGTATTACAGCCCAAGGTTTCTCTACTATTATC 123
DB 427 GAATATTACTGTGTCTACTAATGAAGTATTACAGCCCAAGGTTTCTCTACTATTATC 486
QY 124 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGAAATGTATGGATACAAC 183
DB 487 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGAAATGTATGGATACAAC 546
QY 184 TTACGTTTGTAGAAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTAGTATT 243
DB 547 TTACGTTTGTAGAAAGATTGGGCTTGAAGACCCAGAGATGACATATGCAAGTAGTATT 606
QY 244 TTGTAGAAAGTTGAGGAACCCAGTGTAGTAACTATATTAGGGCGCTGGTGTCTGGTA 303
DB 607 TTGTAGAAAGTTGAGGAACCCAGTGTAGTAACTATATTAGGGCGCTGGTGTCTGGTA 666
QY 304 CTGTACCGGAAAAACAGATTCTTAAAGGAAATCAAATTAGGATAGATTGTATCTGATG 363
DB 667 CTGTACCGGAAAAACAGATTCTTAAAGGAAATCAAATTAGGATAGATTGTATCTGATG 726
QY 364 AATATTTCCTTCTGCAACAGGGTCTGCATCCACTACAAACATTGTTCATGCCACATTCA 423
DB 727 AATATTTCCTTCTGCAACAGGGTCTGCATCCACTACAAACATTGTTCATGCCACATTCA 786
QY 424 CAGAAAGCTGTGAGTCTCTTCAAGTGTACCCCTTCAAGCTTTGCACTGGACCTGTTAATA 483
DB 787 CAGAAAGCTGTGAGTCTCTTCAAGTGTACCCCTTCAAGCTTTGCACTGGACCTGTTAATA 846
QY 484 ATGCTATAATCGCTTTAGTACCTTGGAGACCTTATTTCGATATCTTGAACAGAGAT 543
DB 847 ATGCTATAATCGCTTTAGTACCTTGGAGACCTTATTTCGATATCTTGAACAGAGAT 906
QY 544 GGCAGTTGGACTTAGAAGATCTATATAGCCAACTTGGCAACTCTTGGCAAGGCTTTTG 603
DB 907 GGCAGTTGGACTTAGAAGATCTATATAGCCAACTTGGCAACTCTTGGCAAGGCTTTTG 966
QY 604 TTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGAGGTAAAGATTAT 663
DB 967 TTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGAGGTAAAGATTAT 1026
QY 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGAGAACTAAAGAACCGATA 723
DB 1027 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGAGAACTAAAGAACCGATA 1086
QY 724 CCATTTTCTGCCAGGTTGTCTCCTGGTTAAACGCTGTGGGGAACCTGTGCTGTGTC 783
DB 1087 CCATTTTCTGCCAGGTTGTCTCCTGGTTAAACGCTGTGGGGAACCTGTGCTGTGTC 1146

[illegible]

RESULT 14

ACA04166

ACA01100
ID ACA04166 standard; cDNA; 2849 BP.

XX

AC ACA0

XX

DT 27-MAY-2003 (first entry)

XX

DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 285.

XX

KW Human; ss; gene; secreted protein; transmembrane protein; PRO;

KW inflammatory disease; organ failure; organ failure; atherosclerosis; cardiac injury;

KW infertility; birth defects; premature aging; AIDS; biosensor;

KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 VM hypertension; tumor

KW bioreactor; tumour.
XX

YY	Hom
50	Hom

US HOWO SAPTEMS.
XX

PN
UIS20

:TY-CCT7C0C00Z60 NY

[illegible]

PR	01-DEC-2000;	2000WO-US32678.	CC	diabetic complications. The nucleic acids are useful as hybridisation
PR	20-DEC-2000;	2000WO-US34956.	CC	probes, in chromosome and gene mapping, and in generating antisense RNA
PR	28-FEB-2001;	2001WO-US06520.	CC	or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
PR	01-MAR-2001;	2001WO-US06666.	CC	biosensors or bioreactors. Both are useful in tissue typing.
PR	25-MAY-2001;	2001WO-US17092.	CC	The present sequence encodes a PRO protein of the invention.
PR	01-JUN-2001;	2001WO-US17800.	XX	
PR	20-JUN-2001;	2001WO-US19692.	SQ	Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;
PR	22-JUN-2001;	2001WO-US20116.		
PR	23-JUN-2001;	2001WO-US21056.		
PR	09-JUL-2001;	2001WO-US21735.		
PR	20-DEC-2000;	2000US-0747259.		
PR	28-FEB-2001;	2001US-0796498.		
PR	09-MAR-2001;	2001US-0802706.		
PR	14-MAR-2001;	2001US-0806889.		
PR	22-MAR-2001;	2001US-0816744.		
PR	05-APR-2001;	2001US-0828366.		
PR	10-MAY-2001;	2001US-0854208.		
PR	10-MAY-2001;	2001US-0854280.		
PR	18-MAY-2001;	2001US-0860216.		
PR	25-MAY-2001;	2001US-0866028.		
PR	25-MAY-2001;	2001US-0866034.		
PR	01-JUN-2001;	2001US-0872035.		
PR	05-JUN-2001;	2001US-0874503.		
PR	14-JUN-2001;	2001US-0882636.		
PR	19-JUN-2001;	2001US-0886342.		
PR	21-JUN-2001;	2001US-0887879.		
PR	18-JUL-2001;	2001US-0908827.		
PR	08-AUG-2001;	2001US-0924419.		
PR	09-AUG-2001;	2001US-0927796.		
PR	16-AUG-2001;	2001US-0931836.		
PR	19-DEC-2001;	2001US-0028072.		
XX				
PA	(GETH) GENENTECH INC.			
XX				
PI	Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;			
PI	Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;			
PI	Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;			
XX				
XX	WPI: 2003-331925/31.			
DR	P-PSDB; ABU66988.			
DR				
XX	New secreted and transmembrane nucleic acids and polypeptides,			
PT	designated as PRO, useful for treating inflammation, organ failure,			
PT	atherosclerosis, cardiac injury, infertility, birth defects, premature			
PT	aging, AIDS, or cancer			
XX				
ES	Claim 2; Fig 285; 659pp; English.			
XX				
CC	The invention relates to an isolated nucleic acid comprising, or which is			
CC	at least 80% identical to, or the full-length coding sequence of, any of			
CC	the 275 nucleotide sequences, encoding the corresponding PRO polypeptide			
CC	(one of 275 secreted or transmembrane proteins). The nucleic acid			
CC	further comprises the full-length coding sequence of the DNA deposited			
CC	under American Type Culture Collection (ATCC) accession number in a list			
CC	given in the specification. Also included are vectors and host			
CC	cells for producing PRO proteins, PRO fusion proteins, anti-PRO			
CC	antibodies, PRO extracellular domains and mature sequences, methods			
CC	of detecting PRO proteins, methods for stimulating the release of			
CC	TNF-alpha (tumour necrosis factor alpha) from human blood,			
CC	(and the proliferation of differentiation of chondrocyte cells, the			
CC	proliferation of, or gene expression in pericyte cells, the release or			
CC	proteoglycans from cartilage, proliferation of inner ear utricular			
CC	supporting cells, the proliferation of T-lymphocyte cells, the release			
CC	of a cytokine from peripheral blood mononuclear cells (PBMC), or the			
CC	proliferation of endothelial cells, a method for modulating the uptake			
CC	of glucose or free fatty acid (FFA) by skeletal muscle cells,			
CC	a method for inhibiting the binding of A-peptide to factor VIIA,			
CC	or the differentiation of adipocyte cells, a method for detecting the			
CC	presence of a tumour in a mammal and an oligonucleotide probe derived			
CC	from any of the nucleotide sequences cited above. The nucleic acids and			
CC	polypeptides are useful for treating inflammatory diseases, organ			
CC	failure, atherosclerosis, cardiac injury, infertility, birth defects,			
CC	premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or			

QY	1024	CGTATGCGTTATCTCATCCTTAATCTCAGTCTTTGCTTCAAGGACCTTTCACTTTCAG	1083
Db	1387	CGTATGCGTTATCTCCATCCTTAATCTCAGTCTTTGCTTCAAGGACCTTTCACTTTCAG	1446
QY	1084	GAATTTACAGTGCATTCTGAAAGAGGAGACATCAACAGATTAGGAGTTGTGCAACAGCT	1143
Db	1447	GAATTTACAGTGCATTCTGAAAGAGGAGACATCAACAGATTAGGAGTTGTGCAACAGCT	1506
QY	1144	CTTTTGAGAGGAGGCGCTTAAAGGACAGGAGAAAGGCTCTTCAATCGTGGAAAGAAAATTAA	1203
Db	1507	CTTTTGAGAGGAGGCGCTTAAAGGACAGGAGAAAGGCTCTTCAATCGTGGAAAGAAAATTAA	1566
QY	1204	ATGTTGTATTAAATAGATCAACAGCTAGTTTCAGAGTTACCATGTACGTATTCCTACTAGC	1263
Db	1567	ATGTTGTATTAAATAGATCAACAGCTAGTTTCAGAGTTACCATGTACGTATTCCTACTAGC	1626
QY	1264	TGGGTTCTGTATTTCAGTTCTTTTCGATACGCTTAGGGTAAATGTCAGTACAGGAAAAAA	1323
Db	1627	TGGGTTCTGTATTTCAGTTCTTTTCGATACGCTTAGGGTAAATGTCAGTACAGGAAAAAA	1686
QY	1324	CTGTGCAAGTGAGCACCTGATTCGTTGCCCTTGCTTAACTCTAAAGCTCCATGTCTCTGGG	1383
Db	1687	CTGTGCAAGTGAGCACCTGATTCGTTGCCCTTGCTTAACTCTAAAGCTCCATGTCTCTGGG	1746
QY	1384	CCTAAAAATCGTATAAAAAATCTGGATTCTTTTCTGCTCATATTCAATATGTAA	1443
Db	1747	CCTAAAAATCGTATAAAAAATCTGGATTCTTTTCTGCTCATATTCAATATGTAA	1806
QY	1444	ACCAGAACATTCATGTACTACAAACCTGGTCTTTTAAAGGAACTATGTTGCTATGAAT	1503
Db	1807	ACCAGAACATTCATGTACTACAAACCTGGTCTTTTAAAGGAACTATGTTGCTATGAAT	1866
QY	1504	TAAACTTGCTCATGCTGTAGTACAGACTGGA	1536
Db	1867	TAAACTTGCTCATGCTGTAGTACAGACTGGA	1899

Search completed: November 26, 2003, 00:11:29
Job time : 287.611 secs

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OM nucleic - nucleic search, using sw model

Run on: November 25, 2003, 23:46:56 ; Search time 75.0293 Seconds
(without alignments)
9035.995 Million cell updates/sec

Title: US-09-852-209A-4
Perfect score: 1536
Sequence: 1 cgggtaattccagttttcc.....tgctgtaggacagactgga 1536

Scoring table: IDENTITY NUC
Gapop 10.0 , Capext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1532.6	99.8	2825	4	US-09-040-220D-1
2	1532.6	99.8	2825	4	US-09-265-686-1
3	1511	98.4	1760	4	US-09-564-595D-32
4	1511	98.4	1760	4	US-09-706-368-1
5	1497	97.5	1764	4	US-09-457-066-1
6	955.6	62.2	1095	4	US-09-457-066-50
7	955.6	62.2	1095	4	US-09-706-368-50
8	721	46.9	3571	4	US-09-564-595D-34
9	721	46.9	3571	4	US-09-706-368-42
10	721	46.8	3573	4	US-09-457-066-42
11	684.4	44.6	1035	4	US-09-457-066-6
12	684.4	44.6	1035	4	US-09-706-368-6
13	177.4	11.5	1110	4	US-09-564-595D-6
14	117.4	7.6	1472	4	US-09-540-224-3
15	117.4	7.6	1472	4	US-09-564-595D-52
16	103.6	6.7	1882	4	US-09-540-224-1
17	103.6	6.7	1882	4	US-09-564-595D-1
18	103.6	6.7	1882	4	US-09-706-368-36
19	102.4	6.7	1910	4	US-09-457-066-36
20	40.6	2.6	7218	1	US-08-232-463-14
21	40.6	2.6	40	4	US-09-040-220D-4
22	40	2.6	40	4	US-09-265-686-4
23	37.2	2.4	3098	1	US-08-447-500-1
24	37.2	2.4	3098	1	US-08-454-097-1
25	37.2	2.4	3098	1	US-08-447-408-1
26	37.2	2.4	3098	1	US-08-453-866-1
27	37.2	2.4	3098	3	US-08-185-359-1

28	36.6	2.4	2334	1	US-08-062-632-4	Sequence 4, Appli
c 29	35.2	2.3	29604	3	US-08-781-891-207	Sequence 207, App
c 30	35.2	2.3	29604	4	US-09-618-166-207	Sequence 207, App
c 31	34.6	2.3	3581	2	US-08-738-349-1	Sequence 1, Appli
c 32	34.2	2.2	1201	4	US-09-461-325-36	Sequence 36, Appli
c 33	34.2	2.2	2168	3	US-08-749-522-6	Sequence 6, Appli
c 34	34	2.2	1931	3	US-09-019-942-2	Sequence 2, Appli
c 35	34	2.2	1931	4	US-09-099-041A-1	Sequence 1, Appli
c 36	34	2.2	1931	4	US-09-245-281-1	Sequence 1, Appli
c 37	34	2.2	1931	4	US-09-470-271-2	Sequence 2, Appli
c 38	34	2.2	1931	4	US-09-207-359B-1	Sequence 1, Appli
c 39	34	2.2	1931	4	US-09-340-620A-1	Sequence 1, Appli
c 40	33.8	2.2	10684	3	US-08-618-100B-3	Sequence 3, Appli
c 41	33.8	2.2	1664976	4	US-08-916-421B-1	Sequence 1, Appli
c 42	33.6	2.2	1964	4	US-09-434-613-2	Sequence 2, Appli
c 43	33.6	2.2	1992	1	US-08-455-550-6	Sequence 6, Appli
c 44	33.6	2.2	25002	4	US-08-961-527-48	Sequence 48, Appli
c 45	33.4	2.2	2533	4	US-09-604-605-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-040-220D-1
; Sequence 1, Application US/09040220D
; Patent No. 6391311
; GENERAL INFORMATION:
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC
; TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,
; TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION
; FILE REFERENCE: P1122
; CURRENT APPLICATION NUMBER: US/09/040,220D
; CURRENT FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 1
; LENGTH: 2825
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: Human
; LOCATION: 2689
; OTHER INFORMATION: N is A, T, C or G
US-09-040-220D-1

Query Match	99.8%	Score	1532.6	DB	4	Length	2825
Best Local Similarity	99.9%	Pred. No.	0				
Matches	1532	Conservative	1	Mismatches	0	Indels	0
Gaps	0						
Qy	4	GTAAATCCAGTTTCCAGCAACAGGACAGGAGTACAGATCTCTCAGCATGAGA	63				
Db	341	GTAAATCCAGTTTCCAGCAACAGGACAGGAGTACAGATCTCTCAGCATGAGA	400				
Qy	64	GAATTATTCTGTGTCTACTTAATGGAAGTATTCACAGCCCAAGGTTTCTCATCTTATC	123				
Db	401	GAATTATTCTGTGTCTACTTAATGGAAGTATTCACAGCCCAAGGTTTCTCATCTTATC	460				
Qy	124	CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAC	183				
Db	461	CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAC	520				
Qy	184	TTAGCTTTGATGAAGATTGGGCTTCAGACCCAGAGATGACATATGCAAGTATGATT	243				
Db	521	TTAGCTTTGATGAAGATTGGGCTTCAGACCCAGAGATGACATATGCAAGTATGATT	580				
Qy	244	TTGTAGAGTTGAGGAAACCCAGTGTGAACTATTATTAGGGCGCTGGTGTCTTGTA	303				
Db	581	TTGTAGAGTTGAGGAAACCCAGTGTGAACTATTATTAGGGCGCTGGTGTCTTGTA	640				
Qy	304	CTGTACCAGGAAACAGATTCTTAAGGAAATCAATAGGATAAGATTCTATCTGATG	363				

641	Db	 CTGTACCGGAAACAGATTTCTTAAAGGAATCAAAATTAGGATAAGATTGTATCTGATG	700
364	Qy	AAATATTTCTCTGTAACACAGGGTTCTGTCATCCACTACAACTGTGTATGCCACAATTCA	423
701	Db	AAATATTTCTCTGTAACACAGGGTTCTGTCATCCACTACAACTGTGTATGCCACAATTCA	760
424	Qy	CAGAAGCTGTGAGTCTTCTGATGCTACCCCTTCAGCTTGGCCACTGGACCTGCTTAATA	483
761	Db	CAGAAGCTGTGAGTCTTCTGATGCTACCCCTTCAGCTTGGCCACTGGACCTGCTTAATA	820
484	Qy	ATGCTATAACTGCTTTAGTACCTTGGAGACCTTATTCGATATCTTGAACACAGAGAT	543
821	Db	ATGCTATAACTGCTTTAGTACCTTGGAGACCTTATTCGATATCTTGAACACAGAGAT	880
544	Qy	GGCAGTTGGACTTTAGAAGATCTATATAGGCCAACTTCTGGCAACCTTCTGGCAAGCTTTTG	603
881	Db	GGCAGTTGGACTTTAGAAGATCTATATAGGCCAACTTGGCAACCTTCTGGCAAGCTTTTG	940
604	Qy	TTTTTGAAGAAATCCAGAGTCTGTGATCTGAACCTTCTTAAACAGAGGAGTAAAGATTAT	663
941	Db	TTTTTGAAGAAATCCAGAGTCTGTGATCTGAACCTTCTTAAACAGAGGAGTAAAGATTAT	1000
664	Qy	ACAGCTGCACACCTCGTAACCTTCTAGTGTCCATAAGGGAAGAACTTAAAGAGAACCGATA	723
1001	Db	ACAGCTGCACACCTCGTAACCTTCTAGTGTCCATAAGGGAAGAACTTAAAGAGAACCGATA	1060
724	Qy	CCATTTTCTGGCCAGGTTGTCTCTGTTTAAACGCTGTGCTGGGAACTGTGCTGTGTC	783
1061	Db	CCATTTTCTGGCCAGGTTGTCTCTGTTTAAACGCTGTGCTGGGAACTGTGCTGTGTC	1120
784	Qy	TCCACAATTCGAATGTCAATGTCTCCCAAGCAAAAGTTACTTAAAAATAACCAAGAGG	843
1121	Db	TCCACAATTCGAATGTCAATGTCTCCCAAGCAAAAGTTACTTAAAAATAACCAAGAGG	1180
844	Qy	TCCTTCAGTTGAGACCAAACCGGTGTCAAGGGATTGCACAAATCTACTCACCGACGTGG	903
1181	Db	TCCTTCAGTTGAGACCAAAGCCGGTGTCAAGGGATTGCACAAATCTACTCACCGACGTGG	1240
904	Qy	CCCTGGAGCACCATTGAGGAGTGTACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGC	963
1241	Db	CCCTGGAGCACCATTGAGGAGTGTACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGC	1300
964	Qy	ATCACCAACAGCAGCTCTTCCCGACAGCTGTGCAGTGCAGTGGCTGATTTCTATTAGAGAA	1023
1301	Db	ATCACCAACAGCAGCTCTTCCCGACAGCTGTGCAGTGCAGTGGCTGATTTCTATTAGAGAA	1360
1024	Qy	CGTATGCGTTATCTCCATCTTAACTCAGTTGTTTCTTCAAGGACCTTTTCATCTTCAG	1083
1361	Db	CGTATGCGTTATCTCCATCTTAACTCAGTTGTTTCTTCAAGGACCTTTTCATCTTCAG	1420
1084	Qy	GATTTACAGTGCATTTGAAAGAGGAGACATCAAAACGAATTAGGAGTTGTGCAACAGCT	1143
1421	Db	GATTTACAGTGCATTTGAAAGAGGAGACATCAAAACGAATTAGGAGTTGTGCAACAGCT	1480
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1204	Qy	ATGTTGTATTAAATAGATCAACAGCTAGTTTTCAGAGTTACCATGTACGTATTCACCTAGC	1263
1541	Db	ATGTTGTATTAAATAGATCAACAGCTAGTTTTCAGAGTTACCATGTACGTATTCACCTAGC	1600
1264	Qy	TGGGTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCACTAGCAAGGAAAAA	1323
1501	Db	TGGGTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCACTAGCAAGGAAAAA	1560
1324	Qy	CTGTGCAAGTGAGCACTGATTCGTTTGCCTTGCTTAACTCTAAAGCTCCATGTCTCTGGG	1383
1561	Db	CTGTGCAAGTGAGCACTGATTCGTTTGCCTTGCTTAACTCTAAAGCTCCATGTCTCTGGG	1720
1384	Qy	CCTAAAAATCGTATAAAAATCTGGATTTTTTTTTTTTTTTTTTTTGTCTCATATTCACATATGTAA	1443

Db	1721	CCTAAATCGTAAATCTGGATTTTTTTTTTTTTTGGTCATATTCACATATGTAA	1781
Qy	1444	ACCAGAACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACCTATGTTGCTATGAAT	1503
Db	1781	ACCAGAACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACCTATGTTGCTATGAAT	1840
Qy	1504	TAACTTGTCATGCTGATAGACAGACTGGA	1536
Db	1841	TAACTTGTCATGCTGATAGACAGACTGGA	1873

RESULT 2
 US-09-265-686-1
 ; Sequence 1, Application US/09265686
 ; Patent No. 6455283
 ; GENERAL INFORMATION:
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Kuo, Sophia S.
 ; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMPI
 ; FILE REFERENCE: P1122P2
 ; CURRENT APPLICATION NUMBER: US/09/265,686
 ; CURRENT FILING DATE: 1999-03-10
 ; PRIOR APPLICATION NUMBER: US 09/040,220
 ; PRIOR FILING DATE: 1998-03-17
 ; PRIOR APPLICATION NUMBER: US 09/184,216
 ; PRIOR FILING DATE: 1998-11-02
 ; NUMBER OF SEQ ID NOS: 8
 ; SEQ ID NO 1
 ; LENGTH: 2825
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: Unknown
 ; LOCATION: 2689
 ; OTHER INFORMATION: Any nucleotide
 US-09-265-686-1

Query Match	99.8%;	Score 1532.6;	DB 4;	Length 2825;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1532;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	4	GTAAATCCAGTTTTCCAGCAACAGAGACGGAGTACAAAGATCCCTCAGCATGAGA	63	
Db	341	GTAATTCAGTTTTTCAGCAACAGGAACAGAACGGAGTACAAAGATCCTCAGCATGAGA	400	
Qy	64	GAATTTACTGTGTCCTACTAATGGAAGTATTCACAGCCCCAAGGTTTCCTCATCATTAATC	123	
Db	401	GAATTTACTGTGTCCTACTAATGGAAGTATTCACAGCCCCAAGGTTTCCTCATCATTAATC	460	
Qy	124	CAAGAAATACGGTCTTGATGATGAGATTAGTAGCAGTAGAGGAAATGATGATGATCAAC	193	
Db	461	CAAGAAATACGGTCTTGATGATGAGATTAGTAGCAGTAGAGGAAATGATGATGATCAAC	520	
Qy	184	TTACGTTTGATGAAAGATTTGGGCTTCAAGACCCAGAGATGACATATGCAAGTATGATTT	243	
Db	521	TTACGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATTT	580	
Qy	244	TTGTAGAAGTTGAGGAACCCAGTGTATGGAACATAATTAAGGCGCTGGTGTGGTTATCGGTA	303	
Db	581	TTGTAGAAGTTGAGGAACCCAGTGTATGGAACATAATTAAGGCGCTGGTGTGGTTATCGGTA	640	
Qy	304	CTGTACCAGCAAAACAGATTTCTTAAGGAAATCAAATTAAGGATAAAGATTTGTTATCTGATG	363	
Db	641	CTGTACCAGCAAAACAGATTTCTTAAGGAAATCAAATTAAGGATAAAGATTTGTTATCTGATG	700	
Qy	364	AATATTTTCCTTCTGAACACAGGTTCTGCATCCACTACAACATTTGTATGCCACAATTC	423	
Db	701	AATATTTTCCTTCTGAACACAGGTTCTGCATCCACTACAACATTTGTATGCCACAATTC	760	
Qy	424	CAGAAGCTGTGATGCTCTTCAAGTGCTACCCCTTTAGCTTTGCCACTTGACCTGCTTAATA	483	
Db	761	CAGAAGCTGTGATGCTCTTCAAGTGCTACCCCTTTAGCTTTGCCACTTGACCTGCTTAATA	820	


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QY 484 ATGCTATAAATGCGCTTTAGTACCTTGGAGACCTTTATTCGATATCTTGAACCAAGAGAGAT 543
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QY 821 ATGCTATAAATGCGCTTTAGTACCTTGGAGACCTTTATTCGATATCTTGAACCAAGAGAGAT 880
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QY 544 GGCAGTTGGACTTAGAGATCTATATAGGCCAACTTGCCAACTTCTTGGCAAGCTTTTG 603
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QY 881 GGCAGTTGGACTTAGAGATCTATATAGGCCAACTTGCCAACTTCTTGGCAAGCTTTTG 940
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QY 1181 TCCTTCAGTTGAGACCAAAACCGGTGTCCAGGGATTCACAAATCACTACCGACGTGG 1240
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QY 1241 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGAGCACAGGAGATAGCCGC 1300
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QY 1361 CGTATGGTTATCTCCATCCTTAACTCTCAGTGTGTGCTTCAAGGACCTTTCATCTTCAG 1420
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QY 1084 GATTTACAGTGCATCTTGAAGAGAGAGACATCAAAACAGAAATAGGAGTGTGCAACAGCT 1143
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QY 1421 GATTTACAGTGCATCTTGAAGAGAGAGACATCAAAACAGAAATAGGAGTGTGCAACAGCT 1480
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QY 1144 CTTTGTGAGAGAGCCCTAAAGGACAGGAGAAAAGTCTTCAATCGTGGAAAAGAAAATPAA 1203
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QY 1481 CTTTGTGAGAGAGCCCTAAAGGACAGGAGAAAAGTCTTCAATCGTGGAAAAGAAAATPAA 1540
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QY 1541 ATGTTGTATTAATAGATCACACAGTGTTCAGAGTTACCATGTACGTATTCACACTAGC 1600
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QY 1264 TGGGTTCTGTATTTTCAGTCTTTCGATACGGCTTAGGGTAATGTCAAGTACAGGAAAAAAA 1323
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QY 1601 TGGGTTCTGTATTTTCAGTCTTTCGATACGGCTTAGGGTAATGTCAAGTACAGGAAAAAAA 1660
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QY 1661 CTGTGCAAGTGCACACCTGATTCGGTTCCTTGAATCTTAAGTCCATGTCTCTGGG 1720
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QY 1781 ACCAGAACATTTCTATGTACTACAAACCTGGTTTTTTTAAAAAGGAACATATGTTGCTATGAAT 1840
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QY 1504 TAAACTTGTGTCTGTGATAGGACAGACTGGA 1536
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QY 1841 TAAACTTGTGTCTGTGATAGGACAGACTGGA 1873
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RESULT 3
US-09-564-595D-32
; Sequence 32, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGPF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-09-564-595D-32
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Query Match 98.4%; Score 1511; DB 4; Length 1760;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1522; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
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QY 236 GTAATTTCCAGTCTTTCAGCAACCAAGGAAACAGAACGAGTACAAATCTCTCAGCATGAGA 295
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QY 64 GAAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCTATCTTATTC 123
Db |||||||
QY 296 GAAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCTATCTTATTC 355
Db |||||||
QY 124 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATCTATGGATACAAAC 183
Db |||||||
QY 356 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATCTATGGATACAAAC 415
Db |||||||
QY 184 TTACGTTTGTATGAAAGATTTCGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
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QY 536 CTGTACCAAGGAAAAACAGATTTCCTAAAGGAAATCAAATTAGGATAAGATTTCATCTGATG 595
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QY 596 AATATTTTCTTCTGAAACAGGGTTCTGCATCCCACTACAAATTCATGTCACCAATTCAC 655
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Qy 964 ATCACCAACAGAGCTCTTCCCAAGAGCTGTGAGGAGTGTGAGGAGTGTGAGGAA 1023
Db 1196 ATCACCAACAGAGCTCTTCCCAAGAGCTGTGAGGAGTGTGAGGAGTGTGAGGAA 1255
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RESULT 5

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US-09-457-066-1
; Sequence 1, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEFG3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
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; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-09-457-066-1
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Query Match 97.5%; Score 1497; DB 4; Length 1764;

Best Local Similarity 99.5%; Pred. No. 0;
Matches 1522; Conservative 1; Mismatches 1; Indels 5; Gaps 2;

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Qy 4 GTAAATTCAGTTTCCAGCAACAAAGGACAGAAACGAGTACAAGATCCTCAGCATGAGA 63
Db 236 GTAAATTCAGTTTCCAGCAACAAAGGACAGAAACGAGTACAAGATCCTCAGCATGAGA 295
Qy 64 GAAATTTACTGTGTCTACTTAATGGAAGTATTCACAGCCCAAGGTTTCTCATATTATC 123
Db 296 GAAATTTACTGTGTCTACTTAATGGAAGTATTCACAGCCCAAGGTTTCTCATATTATC 355
Qy 124 CAAGAAATACGCTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAAC 183
Db 356 CAAGAAATACGCTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAAC 415
Qy 184 TTAGCTTTGATGAAGGATTTGGGCTTGAAGACCCAGAAAGATGACATATGCAAGTATGATT 243
Db 416 TTAGCTTTGATGAAGGATTTGGGCTTGAAGACCCAGAAAGATGACATATGCAAGTATGATT 475
Qy 244 TTGTAGAAGTTGAGGAAACCCAGTGTGAAACTATATATAGGCGCTGGTGTCTGTGTA 303
Db 476 TTGTAGAAGTTGAGGAAACCCAGTGTGAAACTATATATAGGCGCTGGTGTCTGTGTA 535
Qy 304 CTGTACCAAGGAAACAGATTTCTAAAGGAAATCAAATTTAGGATAAGATTTGTATCTGATG 363
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Db	CCCTGGAGCACCATGAGGAGTGTCACTGTGTGTGCAGAGGAGACACAGGAGGATAGCCGC	11195
Qy	ATCACCCACGACGCTCTTGCCAGAGCTGTGCAGT---GCAGTGGCTCATTTCTATTAG	1019
Db	ATCACCCACGACGCTCTTGCCAGAGCTGTGCAGTLYLYGCAGTGGCTCATTTCTATTAG	12555
Qy	AGAACTGATGCGTTATCTCCATCCTTAATCTCACTGTGTGTTCCTTCAAGGACCTTTCACTCT	1079
Db	AGAACTGATGCGTTATCTCCATCCTTAATCTCACTGTGTGTTCCTTCAAGGACCTTTCACTCT	1315
Qy	TCAGGATTACAGTGCATTCGAAAGAGGAGACATCAAAAGATTTAGGAGTTGTGCAAC	1139
Db	TCAGGATTACAGTGCATTCGAAAGAGGAGACATCAAAAGATTTAGGAGTTGTGCAAC	1375
Qy	AGCTCTTTTGAGAGGAGCGCTTAAAGGACAGGAGAAAAAGTCTTCAATCTGTGGAAAAAGAAA	1199
Db	AGCTCTTTTGAGAGGAGCGCTTAAAGGACAGGAGAAAAAGTCTTCAATCTGTGGAAAAAGAAA	1435
Qy	TTAAATGTGTATTAAATAGATACACGCTAGTTTCAGAGTTACCATGTACGTTATCCAC	1259
Db	TTAAATGTGTATTAAATAGATACACGCTAGTTTCAGAGTTACCATGTACGTTATCCAC	1495
Qy	TAGCTGGGTCTGTATTTCACTTCTTCGATACGCGCTTAGGGTAAATCTCAGTACAGGAAA	1319
Db	TAGCTGGGTCTGTATTTCACTTCTTCGATACGCGCTTAGGGTAAATCTCAGTACAGGAAA	1555
Qy	AAAACTGTGCAAGTGAGCACCTGAATCCGTTGCCCTTAACTCTAAAGCTCCATGTCC	1379
Db	AAAACTGTGCAAGTGAGCACCTGAATCCGTTGCCCTTAACTCTAAAGCTCCATGTCC	1615
Qy	TGGGCTTAAATCGTATAAAACTGTGGA-TTTTTTTTTTTTTTTTTTTTGGCTCATATTCACATA	1438
Db	TGGGCTTAAATCGTATAAAACTGTGGA-TTTTTTTTTTTTTTTTTTTTGGCTCATATTCACATA	1675
Qy	TGTAAAACAGAACTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTCCTA	1498
Db	TGTAAAACAGAACTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTCCTA	1735
Qy	TGAATTTAACTTTGTGTCATGCTGATAGGA	1527
Db	TGAATTTAACTTTGTGTCATGCTGATAGGA	1764

D5	722	TTTTTGGAGAGAAAATCAGAGTGGTGGATCTGAACCTTCTAAACAGAGAGGTAAGATAT	781
QY	664	ACAGCTGCACACCTCGTAACCTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGGATA	723
D5	782	ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGGATA	841
QY	724	CCATTTTCTGGCCAGGTTGTCTCTCGTTAAACGCTGTGTGGGAACTGTGCCCTGTGTGC	783
D5	842	CCATTTTCTGGCCAGGTTGTCTCTCGTTAAACGCTGTGTGGGAACTGTGCCCTGTGTGC	901
QY	784	TCCCAATTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTTACTTAAAAATTACCACGAGG	843
D5	902	TCCCAATTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTTACTTAAAAATTACCACGAGG	961
QY	844	TCCTTTCAGTTGAGACCAAAACCGGTGTACGGGGATTGCACAAATCACTCACCGACGTGG	903
D5	962	TCCTTTCAGTTGAGACCAAAACCGGTGTACGGGGATTGCACAAATCACTCACCGACGTGG	1021
QY	904	CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGGGGAGCACAGGAGGATAG	959
D5	1022	CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGTGCAGGGGAGCACAGGAGGATAG	1077

RESULT 7
US-09-706-968-50
; Sequence 50, Application US/09706968
; Patent No. 6528050

```

; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 50
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fused DNA
US-09-706-968-50

Query Match      62.2%; Score 955.6; DB 4; Length 1095;
Best Local Similarity 99.9%; Pred. No. 9.8e-259;
Matches 955; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      4  GTAATTTCCAGTTTTCAGACCAACAGGACAGAGGATACAGATCCCTCAGCATGAGA 63
Db      122  GTAATTTCCAGTTTTCAGACCAACAGGACAGAGGATACAGATCCCTCAGCATGAGA 181

Qy      64  GAATTTATCTGTCTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATCTTATC 123
Db      182  GAATTTATCTGTCTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATCTTATC 241

Qy      124  CAAGAAATACGGTCTTGGTATGGAGATAGTAGCAGTAGAGAGAAATGTGGATACAAC 183
Db      242  CAAGAAATACGGTCTTGGTATGGAGATAGTAGCAGTAGAGAGAAATGTGGATACAAC 301

Qy      184  TTACGTTTGATGAAGATTTCGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
Db      302  TTACGTTTGATGAAGATTTCGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 361

Qy      244  TTGTAGAAGTTGAGGAACCCAGTGTATGGAACATATATTAGGCGCTGGTGTGGTTCTGTA 303
Db      362  TTGTAGAAGTTGAGGAACCCAGTGTATGGAACATATATTAGGCGCTGGTGTGGTTCTGTA 421

Qy      304  CTGTACCAAGAAACAGATTTCCTAAAGAAATCAAATTTAGGATTAAGATTTCATCTGATG 363
Db      422  CTGTACCAAGAAACAGATTTCCTAAAGAAATCAAATTTAGGATTAAGATTTCATCTGATG 481

Qy      364  AATATTTTCTCTTGAACACAGGTTTCTGCATCCACTACACATTTGTCTATGCCACAATTC 423
Db      482  AATATTTTCTCTTGAACACAGGTTTCTGCATCCACTACACATTTGTCTATGCCACAATTC 541

Qy      424  CAGAAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTTGGCAGCTGCTGTTAATA 483
Db      542  CAGAAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTTGGCAGCTGCTGTTAATA 601

Qy      484  ATGCTATTAACCTGCTTTAGTACCTTGGAGACCTTATTTCGATATCTTCAACACAGAGAT 543
Db      602  ATGCTATTAACCTGCTTTAGTACCTTGGAGACCTTATTTCGATATCTTCAACACAGAGAT 661

Qy      544  GCGAGTTGGACTTAGAAGATCTATATAGGCCAACTTTGGCACTTCTTGGCAAGGCTTTTG 603
Db      662  GCGAGTTGGACTTAGAAGATCTATATAGGCCAACTTTGGCACTTCTTGGCAAGGCTTTTG 721

Qy      604  TTTTGGAGAAATTCAGAGTGGTGGATCTGAACTTCTTAACAGAGAGGTAAAGATTAT 663
Db      722  TTTTGGAGAAATTCAGAGTGGTGGATCTGAACTTCTTAACAGAGAGGTAAAGATTAT 781

Qy      664  ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGGAAGAACTAAGAGAACCGATA 723
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Db      782  ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGGAAGAACTAAGAGAACCGATA 841
Qy      724  CCATTTTCTGSCCAGGTTGTCTCTCTGTTTAAACGCTGTGTGGAACTGTGCTGTTGTC 783
Db      842  CCATTTTCTGSCCAGGTTGTCTCTCTGTTTAAACGCTGTGTGGAACTGTGCTGTTGTC 901
Qy      784  TCACAAATTCGAATGAATGTCAATGTGTCCTCCACGAAAGTTACTAAAAATACCAAGG 843
Db      902  TCACAAATTCGAATGAATGTCAATGTGTCCTCCACGAAAGTTACTAAAAATACCAAGG 961
Qy      844  TCCTTCAGTTGAGACCAAAACACCGGTGTCAAGGGAATTCACAAATCACTCAACGACGTGG 903
Db      962  TCCTTCAGTTGAGACCAAAACACCGGTGTCAAGGGAATTCACAAATCACTCAACGACGTGG 1021
Qy      904  CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGGATAG 959
Db      1022  CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGGATAG 1077

RESULT 8
US-09-564-595D-34
; Sequence 34, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 3571
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1049)...(2086)
US-09-564-595D-34

Query Match      46.9%; Score 721; DB 4; Length 3571;
Best Local Similarity 83.6%; Pred. No. 1.4e-192;
Matches 817; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

Qy      4  GTAATTTCCAGTTTTCAGACCAACAGGACAGAGGATACAGATCCCTCAGCATGAGA 63
Db      1131  GCAAGTTCGACGCTCTCCAGCGACAGAGACAGAGGATGCAAGATCCCGCATGAGA 1190

Qy      64  GAATTTATCTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATATCTTATC 123
Db      1191  GAGTTGTCACTATATCTGTTAATGGAGCATCCACAGCCCAAGTTTCTCATATACATACC 1250

Qy      124  CAAGAAATACGGTCTTGGTATGGAGATAGTAGCAGTAGAGAGAAATGTATGATACAC 183
Db      1251  CAAGAAATATGGTGTGCTGGTGTGGAGATTAGTTGCAAGTAGAGTAAATGTGCGGATCCAGC 1310

Qy      184  TTACGTTTGATGAAGATTTCGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
Db      1311  TGACATTTGATGAGGATTTGGCTTGAAGATCCAGAGACGATATATGCAAGTATGATT 1370

Qy      244  TTGTAGAAGTTGAGGAACCCAGTGTATGGAACCTATATTAGGCGCTGGTGTGGTTCTGTA 303
Db      1371  TTGTAGAAGTTGAGGAGCCAGTGTATGGAAGTGTGTTTATAGGACGCTGGTGTGGTTCTGGA 1430
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QY 964 ATCACCACGAGCCTC 980
Db 2091 AGCCTTCGTAGCAGCAC 2107

RESULT 10
US-09-457-066-42
; Sequence 42, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 3571
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1049)...(2086)
US-09-457-066-42

Query Match 46.9%; Score 721; DB 4; Length 3573;
Best Local Similarity 83.6%; Pred. No. 1.4e-192;
Matches 817; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 4 GTAAATTCAGTTTCCAGCAGCAGGAGCAGGAGTACAGATCCTCAGCATGAGA 63
Db 1131 GCAAGTTTGCAGCTCTCCAGCAGCAGGAGCAGGAGTACAGATCCTCAGCATGAGA 1190
QY 64 GAATATTAATCTGCTCTACTTAATGAGTATTCACAGCCCAAGTTTCTCATACTTATC 123
Db 1191 GAGTTGTCATATATCTGTTATGGAGATCCACAGCCCAAGTTTCTCATACTTATC 1250
QY 124 CAAGAAATACGCTCTTGATGAGATTTAGTACAGTACAGGAGGAGGAGTATGAGTACAA 183
Db 1251 CAAGAAATATGCTGCTGTTGGAGATTTAGTTGAGTATGAGGAGGAGTATGAGTACAA 1310
QY 184 TTACGTTTGTAGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
Db 1311 TGACATTTGTATGAGAGATTTGGGCTTGAAGATCCAGAGACGATATATGCAAGTATGATT 1370
QY 244 TTGTAGAAGTTGAGGAGCAGGATGAGGAGTATATATAGGCGCTGGTGTGTTCTGTGTA 303
Db 1371 TTGTAGAAGTTGAGGAGCAGGATGAGGAGTATATAGGCGCTGGTGTGTTCTGTGGA 1430
QY 304 CTGTACAGGAGGAGGAGTATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 363
Db 1431 CTGTGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1490
QY 364 AATATTTTCTCTGAGCAGGAGTCTGCATCCCTACACATGATTCATGCGCAGGAGTCA 423
Db 1491 AGTATTTTCCATCTGAGCAGGAGTCTGCATCCCTACACATGATTCATGCGCAGGAGTCA 1550
QY 424 CAGAGCTGTGAGTCTCTGAGTGTGCTACCCCTTACAGCTTTGCGCTGAGCTGCTTATA 483
Db 1551 CAGAAACCAAGGAGTCTCTGAGTGTGCTACCCCTTACAGCTTTGCGCTGAGCTGCTTATA 1610
QY 484 ATGCTATAATGCTCTTATGATCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 543
Db 1611 ATGCTGTGAGTCTCTGATGATCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1670
QY 544 GGCAGTTGGAGCTTAGAGATCTATATAGGCCAAGTCTGCGCAAGCTCTTGGCAAGGCTTTG 603

1671 GGAGGTGGAGTTCGAGCAGCTCTTACAAAGCCACATGGCAGCTTTTGGGCAAGGCTTTCC 1730
604 TTTTGGAGAGAAATCCAGAGTGTGTGATCTGAACCTTTCTAAACAGAGAGGAGTAAAGATTAT 663
1731 TGTATGGGAGAGAGAGCAGAGTGTGTGATCTGAATCTCTCAAGAGAGAGGTAAGACTCT 1790
664 ACAGCTGCACACCTCTGTAATCTTCTAGTGTCCATTAAGGAGAGAGCTAAAGAGACCGATA 723
1791 ACAGCTGCACACCCCGGAACTTCTAGTGTCCATTAAGGAGAGAGCTAAAGAGGACAGATA 1850
724 CCATTTTCTGCGCAGGTTGCTCTCTGCTTAAACCTGTGGGAGTCTGCTGCTGCTGCTGCT 783
1851 CCATATTTCTGCGCAGGTTGCTCTCTGCTTAAACCTGTGGAGGAGTCTGCTGCTGCTGCT 1910
784 TCCATATTCGATGAATGTCAATGTGTCCCAAGCAAGTTTACTTAAATAATACCAAGAGG 843
1911 TCCATATTCGATGAATGTCAATGTGTCCCAAGCAAGTTTACTTAAATAATACCAAGAGG 1970
844 TCCATATTCGATGAATGTCAATGTGTCCCAAGCAAGTTTACTTAAATAATACCAAGAGG 903
1971 TCCATATTCGATGAATGTCAATGTGTCCCAAGCAAGTTTACTTAAATAATACCAAGAGG 2030
904 CCCTGGAGCAGCAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 963
2031 CTCTGGAGCAGCAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2090
964 ATCACCACGAGCCTC 980
2091 AGCCTTCGTAGCAGCAC 2107

RESULT 11
US-09-457-066-6
; Sequence 6, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: degenerate sequence derived from SEQ ID NOS: 1 and
; OTHER INFORMATION: 2
; NAME/KEY: misc feature
; LOCATION: (1)-(1035)
; OTHER INFORMATION: n = A,T,C or G
US-09-457-066-6

Query Match 44.6%; Score 684.4; DB 4; Length 1035;
Best Local Similarity 57.5%; Pred. No. 1.5e-182;
Matches 547; Conservative 239; Mismatches 166; Indels 0; Gaps 0;

QY 4 GTAAATTCAGTTTCCAGCAGCAGGAGTACAGATCCTCAGCATGAGA 63
Db 83 SNAARTTVCARTTWSNWSNAAVAARGARCAAAVGGNGTNCARGAYCCNCAACAYGARM 142
QY 64 GAATATTAATCTGCTCTACTTAATTCAGAGGAGTATTCAGAGGAGGAGTCTCTCATATCATC 123
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Db 143 GNATHATHACNGTWSNACNAAYGNGWSNATHCAYWSNCCNMGNTTCCNAYACNTAYC 202
Qy 124 CAAGAATACGGTCTTGATGAGATTTAGTACAGTAGAGGAAATGATGATGATCAAC 183
Db 203 CNMGNAAACNGTNYTNGTNGMNGTNGTNGCNGTNGARGAAYGNTNGATHCARY 262
Qy 184 TTACGTTTGTATGAAGATTTGGGCTTGAAGACCAGAGATGACATATGCAAGTATGAT 243
Db 263 TNACNTTGTAGGARMGNTTGGNYTNGARGAYCNGARGAYGAVATHTGYAARTAYGAT 322
Qy 244 TTGTAGAGTTGAGAACACCGAGTGGAACTATATATAGGGCGCTGGTGGTCTGGTA 303
Db 323 TYGTNGARGTNGARGARCCNWSNGAYGNAACNATHYTNMGNTGGTGYGWSNGNA 382
Qy 304 CTGTACAGGAAACAGATTTCTAAAGGAAATCAAAATAGGATAAGATTTGTATCTGATG 363
Db 383 CNGTNCNCGNNAARCARATHWSNARGNAAYCARATHMGNATHMGNNTTGTWSNGAYG 442
Qy 364 AATATTTTCTCTGAACACCGGTTCTGACCTTCCACTCAACATTTGTCATGCCCAATTC 423
Db 443 ARTAYTTCCNWSNGARCCNGGNTTGTGATHCAYATAYAAVATHTGNATGCCNCARTYA 502
Qy 424 CAGAGCTGTGAGTCTTCTAGTGTACCCCTTACGCTTTGACCTGACCTGCTGTTAATA 483
Db 503 CNGARGCNGTWSNCCNWSNGTNYTNCNCCNWSNGNYTNCNNTNGAYTNTYNAAYA 562
Qy 484 ATGTATAACTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACACGAGAGAT 543
Db 563 AYGCNATHACNGNTTWSNACNYTNGARGAYTNTATHMGNATYTNARGCNGARGMNT 622
Qy 544 GGCAGTTTGGACTTAGAAGATCTATATAGGCAACTTGGCAACTCTTGGCAAGCTTTTG 603
Db 623 GGCARYTNGAYTNGARGAYTNTAYMGNCCNACNTGGCARYTNTYNGNNAARGCNTTYG 682
Qy 604 TTTTGAAGAAATCCAGAGTGTGATCTGACCTTCTAAGAGGAGGTGAAGTAT 663
Db 683 TNYTNGMNAARWSNMGNTNGTNGAYTNTAYMGNCCNACNTGGCARYTNTYNGNNAARGCNTTYG 742
Qy 724 CCATTTCTGCCAGGTGCTCTCGTTAAACCTGTGTGGAACCTGTGCGCTGTGTGTC 783
Db 803 CNAHTTCTGCCNGGNTGYTNTYTNATMGNMNTGYGNGGNAAYTGYGNTGYTGY 862
Qy 784 TCCAAATTCGAATGATGTCATGTCCTCAAGCAAGTACTTAAAGAAATACACGAG 843
Db 863 TNCAYAAATGYAAGTGTGARTGYGTGTCNCCNWSNARGTNCAYARWSNTNACNGAYTNG 922
Qy 844 TCCTTCAGTTGAGACCAAAACCGGTGTGAGGGGATTCGACAAATCACTCACCGACGTGG 903
Db 923 TNYTNCARYTNGMNCNNAARACNGGNTNGMNGNYTNCAYARWSNTNACNGAYTNG 982
Qy 904 CCTGTGAGCACCATGAGAGTGTGACTGTGTGTCAGAGGAGGACACGAGG 955
Db 983 CNYTNGARCAAYCAYGARGARTGYGTYGNTGTNGMNGGWSNACNGGNGG 1034
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RESULT 12

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US-09-706-968-6
; Sequence 6, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
```

```
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: degenerate sequence derived from SEQ ID NOS: 1 and
; OTHER INFORMATION: 2
; NAME/KEY: misc.feature
; LOCATION: (1)...(1035)
; OTHER INFORMATION: n = A, T, C or G
; US-09-706-968-6
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Query Match 44.6%; Score 684.4; DB 4; Length 1035;
Best Local Similarity 57.5%; Pred. No. 1.5e-182;
Matches 547; Conservative 239; Mismatches 166; Indels 0; Gaps 0;
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Qy 4 GTAAATCCAGTTTCCAGCAACAGGAACAGAACCGAGTACAGATCCTCCAGCATCAGA 63
Db 83 SNAARTTYCARTTYSWSNAAAYAAARGARCARAAYGNGTNCARGATCCNARCAIYARM 142
Qy 64 GAATATTTACTGTGTCTACTAATGGAAGATTTACAGCCCAAGGTTTCTCATCTTATC 123
Db 143 GNATHATHACNGTWSNACNAAYGNGWSNATHCAYWSNCCNMGNTTCCNAYACNTAYC 202
Qy 124 CAAGAATACGGTCTTGATGAGATTTAGTACAGTAGAGGAAATGATGATGATCAAC 183
Db 203 CNMGNAAACNGTNYTNGTNGMNGTNGTNGCNGTNGARGAAYGNTTGGATHCARY 262
Qy 184 TTACGTTTGTAGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGAT 243
Db 263 TNACNTTGTAGARMGNTTGGNYTNGARGAYCNGARGAYGATHTGYAARTAYGAT 322
Qy 244 TTGTAGAAAGTTGAGAACCCAGAGTGTGAACTATATTTAGGGCGCTGGTGGTCTGGTA 303
Db 323 TYGTNGARGTNGARGARCCNWSNGAYGNAACNATHYTNMGNTGGTGYGWSNGNA 382
Qy 304 CTGTACAGGAAACAGATTTCTAAAGGAAATCAAAATAGGATAAGATTTGTATCTGATG 363
Db 383 CNGTNCNCGNNAARCARATHWSNARGNAAYCARATHMGNATHMGNNTTGTWSNGAYG 442
Qy 364 AATATTTTCTCTGACAGGTTCTGACCTTCAAGCAAGTACTTAAAGAAATACACGAG 423
Db 443 ARTAYTTCCNWSNGARCCNGGNTTGTGATHCAYATAYAAVATHTGNATGCCNCARTYA 502
Qy 424 CAGAGCTGTGAGTCTTCTAGTGTACCCCTTACGCTTTGACCTGACCTGCTTAAATA 483
Db 503 CNGARGCNGTWSNCCNWSNGTNYTNCNCCNWSNGNYTNCNNTNGAYTNTYNAAYA 562
Qy 484 ATGTATAACTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACACGAGAT 543
Db 563 AYGCNATHACNGNTTWSNACNYTNGARGAYTNTATHMGNATYTNARGCNGARGMNT 622
Qy 544 GGCAGTTTGGACTTAGAAGATCTATATAGGCAACTTGGCAACTCTTGGCAAGGCTTTTG 603
Db 623 GGCARYTNGAYTNGARGAYTNTAYMGNCCNACNTGGCARYTNTYNGNNAARGCNTTYG 682
Qy 604 TTTTGAAGAAATCCAGAGTGTGATCTGACCTTCTAAGAGGAGGTGAAGTAT 663
Db 683 TNYTNGMNAARWSNMGNTNGTNGAYTNTAYMGNCCNACNTGGCARYTNTYNGNNAARGCNTTYG 742
Qy 724 CCATTTCTGCCAGGTGCTCTCGTTAAACCTGTGTGGAACCTGTGCGCTGTGTGTC 783
Db 803 CNAHTTCTGCCNGGNTGYTNTYTNATMGNMNTGYGNGGNAAYTGYGNTGYTGY 862
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QY 54 CAGCATGAGAAATATTACTGTCTACTAATGGAAGTATTACAGGCCCAAGTTTCCT 113
DB 243 CAGAGAGAGAGAAACATTCAGGTGACAGCAATGGCCATGTGAGAGTCTCGCTTCCCG 302
QY 114 CATACTTATCCAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTA 173
DB 303 AACAGTACCCAGGAACTGCTTCTGACATGCTGGTCCGTTTC---CCAGGAGAAACA 359
QY 174 TGGATACAACTTACGTTTGTATGAAAGATTGGCTTGAAGCCAGAACGATGATATGC 233
DB 360 CGGATACAACTGTCTTTCACCATCAATTGGGACTAGAGGAGACAGAAATGCAATTTGT 419
QY 234 AAGTATGATTGTGTAAGTTGAGAACCCAGTATGAA-----CTATATTAGGGCGC 287
DB 420 AGGTATGACTTGTGGAAGTTGAGAACTCTCAGAGAGCAGCACTGTGTGAGAGGAGA 479
QY 288 TGGTGTGCTTCTGCTACTGTACAGGAAACACAGATTCTAAAGGAAATCAAAATTAGGATA 347
DB 480 TGGTGTGCCCACAGGAGATCCCTCCAGGATACGTCAGAACCAACAGATTAAATC 539
QY 348 AGATTGTATCTGATGAATATTTTCTTCTGAAACGAGGTTCTGCATCCACTACAACTT 407
DB 540 ACATTTAAGTCTGATGACTACTTGTGCAAAACCTCGAATTCAGGATTTATTTCAATT 599
QY 408 GT----CATGCCAAATTCAGAGTGTGAGTCTTCACTGTCTACCCCTTCAGCTTT 463
DB 600 GTGGAAGATTTCCAAACCGGAGAGCCTCAGAGACCAACTGGGAATCAGTCACAGCTCT 659
QY 464 GCCACTGCACCTGCTTA----- 480
DB 660 TTCTCTGGGGTGTCTTATCACTCTCCATCAATACGGACCCCACTCTCACTGCTGATGCC 719
QY 481 ----ATAATGCTATACTGCCCTTTAGTACCTTGGAGAGACCTTATTCGATATCTTGAACCA 536
DB 720 CTGGACAAAACGTGCGAGAAATTCGATACCGCTGGAAGATCTTACTTAAGCACTTCAATCCA 779
QY 537 GAGAGATGGCAGTTGGACTTAGAGATCTATATAGGCCCACTTGGCACTTCTTGGCAAG 596
DB 780 GTGTCTTGGCAAGATGATCTGGGAATTTGATCTGGACACCCCTCATTTAGAGGAGG 839
QY 597 GCTTTTGTGTTTGGAGAAATCCAGAGTGTGTGATCTGAACTTCTTAAACAGAGAGGATA 656
DB 840 TCATACCATGATCGGA-----AGTCCAAAGTGGACCTGGACAGGCTCAATGATGATGTC 893
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DB 894 AAGGTTTACAGTTGCATCCAGGAATCACTTCTGTGAACCTCAGGGAGGAGCTGAGCTG 953
QY 717 ACCGATACCAATTTCTGGCCAGGTTGTCTCTGTTTAAACGCTGTGTGGAACTGTGCC 776
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QY 777 TGTGTCTCCCAATTCGAATGAATGTAATGTGTCCCAAGCAAAAGTTACTTAAATAATAC 836
DB 1014 TGGGGAATGTCATCTGGAAGTCTGTCATGTCAGCTCAGGGAAGACAGTGAAGAGTAT 1073
QY 837 CACGAGGTCTTCACTGTGAGACC-----AAASACCGTGTGAGGGGATTCACAAA 887
DB 1074 CATGAGTATTGAAGTTGAGCTGGACATTTCAAGAGAAGGGCAAGCTAAGATATG 1133
QY 888 TCATCTACCGAGCTGGCCCTGGAGCAACATGAGGAGTGTGATCTGTGTGAGAGGGAGC 947
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QY 948 ACAGAGAGATA 958
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RESULT 15

US-09-564-595D-52

; Sequence 52, Application US/09564595D

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; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles B.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)...(1205)
; US-09-564-595D-52
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Query Match 7.6%; Score 117.4; DB 4; Length 1472;
Best Local Similarity 50.8%; Pred. No. 3.4e-23;
Matches 493; Conservative 1; Mismatches 402; Indels 75; Gaps 6;
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QY 174 TGGATACAACTTACGTTTGTATGAAAGATTGGGCTTGAAGCCAGAACGATGATATGC 233
DB 360 CGGATACAACTGTCTTTCACCATCAATTGGGACTAGAGGAGACAGAAATGCAATTTGT 419
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DB 420 AGGTATGACTTGTGGAAGTTGAGAACTCTCAGAGAGCAGCACTGTGTGAGAGGAGA 479
QY 288 TGGTGTGCTTCTGCTACTGTACAGGAAACACAGATTCTAAAGGAAATCAAAATTAGGATA 347
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QY 481 ----ATAATGCTATACTGCCCTTTAGTACCTTGGAGAGACCTTATTCGATATCTTGAACCA 536
DB 720 CTGGACAAAACGTGCGAGAAATTCGATACCGCTGGAAGATCTTACTTAAGCACTTCAATCCA 779
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Qy 1074 CATGAGGTATTGAAGTTTGAGCCTGGACATTTCAAGAGAAGGGGCAAAAGCTTAAGATATG 1133
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Qy 1134 GCTCTTGTGTATCCAGCTGGATCATCATGAGCGATGTGACTGTATCTGCAGCTCAAGA 1193
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Job time : 81.0293 secs

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OM nucleic - nucleic search, using sw model

Run on: November 26, 2003, 03:42:52 ; Search time 378.148 Seconds
(without alignments)
13382.717 Million cell updates/sec

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Perfect score: 1536
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	1535.6	100.0	1536	14	Sequence 4, Appli
3	1532.6	99.8	2825	14	US-10-131-600-4
4	1532.6	99.8	2849	10	US-10-178-442-1
5	1532.6	99.8	2849	10	US-09-978-295A-487
6	1532.6	99.8	2849	10	US-09-978-697-487
7	1532.6	99.8	2849	10	US-09-978-192A-487
8	1532.6	99.8	2849	11	US-09-999-832A-487
9	1532.6	99.8	2849	11	US-09-978-189-487
10	1532.6	99.8	2849	11	US-09-978-608A-487
11	1532.6	99.8	2849	11	US-09-978-585A-487
12	1532.6	99.8	2849	11	US-09-978-191A-487
13	1532.6	99.8	2849	11	US-09-978-403A-487
14	1532.6	99.8	2849	11	US-09-978-564A-487
15	1532.6	99.8	2849	11	US-09-999-833A-487
16	1532.6	99.8	2849	11	US-09-981-915A-487
17	1532.6	99.8	2849	11	US-09-978-824-487

17	1532.6	99.8	2849	11	US-09-918-585A-487	Sequence 487, App
18	1532.6	99.8	2849	11	US-09-978-423A-487	Sequence 487, App
19	1532.6	99.8	2849	11	US-09-978-193A-487	Sequence 487, App
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21	1532.6	99.8	2849	11	US-09-978-757A-487	Sequence 487, App
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24	1532.6	99.8	2849	12	US-09-978-375A-487	Sequence 487, App
25	1532.6	99.8	2849	12	US-09-978-188A-487	Sequence 487, App
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27	1532.6	99.8	2849	12	US-10-137-870-285	Sequence 285, App
28	1532.6	99.8	2849	12	US-10-140-018-285	Sequence 285, App
29	1532.6	99.8	2849	12	US-10-140-021-285	Sequence 285, App
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39	1532.6	99.8	2849	12	US-10-142-421-285	Sequence 285, App
40	1532.6	99.8	2849	12	US-10-142-432-285	Sequence 285, App
41	1532.6	99.8	2849	12	US-10-142-767-285	Sequence 285, App
42	1532.6	99.8	2849	12	US-10-143-031A-487	Sequence 487, App
43	1532.6	99.8	2849	12	US-10-143-033-285	Sequence 285, App
44	1532.6	99.8	2849	12	US-10-144-994-285	Sequence 285, App
45	1532.6	99.8	2849	12	US-10-145-628-285	Sequence 285, App

ALIGNMENTS

RESULT 1
US-09-852-209A-4
; Sequence 4, Application US/09852209A
; Patent No. US20020164687A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT FILING DATE: 2001-05-10
; PRIOR FILING DATE: 1999-09-30
; PRIOR FILING DATE: 1998-12-03
; PRIOR FILING DATE: 1998-12-18
; PRIOR FILING DATE: 1998-12-18
; PRIOR FILING DATE: 1999-05-21
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-852-209A-4
Query Match 100.0%; Score 1535.6; DB 10; Length 1536;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Qy	61	AGAGAATATTACTGTGTCTACTAAATGGAAGTATTCACAGCCCAAGGTTTCCCTCATACTT	120
Db	61	AGAGAATATTACTGTGTCTACTAAATGGAAGTATTCACAGCCCAAGGTTTCCCTCATACTT	120
Qy	121	ATCCAGAAATACCGTCTTCGTATGAGATATGATGAGATAGAGAAATGTATGATAC	180
Db	121	ATCCAGAAATACCGTCTTCGTATGAGATATGATGAGATAGAGAAATGTATGATAC	180
Qy	181	AACCTAGCTTGTATGAAGATTTGGGCTTCAGACCCAGAGATGACATATGCAAGTATG	240
Db	181	AACCTAGCTTGTATGAAGATTTGGGCTTCAGACCCAGAGATGACATATGCAAGTATG	240
Qy	241	ATTTTGTAGAGTTGAGAACCCAGTGTATGAACTATATAGGCGCTGGTGTGTTCTG	300
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Qy	301	GTACTGTACAGGAAACAGATTTCTAAGAAATCAAATAGGATTAAGATTTGTATCTG	360
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Db	361	ATGAATATTTTCTTCTGAACAGGTTCTGCATCCACTCAACATTTGTATGCAACAAT	420
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Db	481	ATAATGCTATAACTGCTTTAGTACCTTGGAGACCTTATTCGATATCTTGAACACAGA	540
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Db	541	GATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTCTTGGCAAGGCTT	600
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Db	721	ATACCATTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGTGGGAACCTGTGCTGTT	780
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Db	841	AGGTCTTTCAGTTCAGACCAAAACCGGTGTGAGGATTCACAAATCACTCACCGACG	900
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Qy	1201	TAAATGTGTATTAAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTATTTCCACT	1260
Db	1201	TAAATGTGTATTAAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTATTTCCACT	1260
Qy	1261	AGCTGGGTTCTGTATTTTCAGTTCCTTCGATACGGCTTAGGTAATGTACAGTACAGGAAA	1320
Db	1261	AGCTGGGTTCTGTATTTTCAGTTCCTTCGATACGGCTTAGGTAATGTACAGTACAGGAAA	1320
Qy	1321	AACTGTGCAAGTAGACACCTGATTCCTGCTTCCCTTAACTCTAAAGCTCCATGCTCT	1380
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Qy	1381	GGGCTAAATTCGTATATAAATCTGGATTTTCTGCTCATATTCACATATG	1440
Db	1381	GGGCTAAATTCGTATATAAATCTGGATTTTCTGCTCATATTCACATATG	1440
Qy	1441	TAAACCAAGAACATTTCTATGTAATAACCAACCTGGTTTTTAAAGGAACTATGTTGCTATG	1500
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RESULT 2

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; Sequence 4, Application US/10131600
; Publication No. US20030082670A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/10/131,600
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-600-4

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QY	721	ATACATTTTCTGGCCAGGTTGTCTCTGTTTAAACGCTGTGTTGGGAACTGTGCTGTT	780		
DB	721	ATACATTTTCTGGCCAGGTTGTCTCTGTTTAAACGCTGTGTTGGGAACTGTGCTGTT	780		
QY	781	GTCTCCCAATTTGCAATGCTCAATGTCTCCAGCAAGTGTACTTAAATAATACCAG	840		
DB	781	GTCTCCCAATTTGCAATGCTCAATGTCTCCAGCAAGTGTACTTAAATAATACCAG	840		
QY	841	AGGTCTCTCAGTTGAGACCAASACCGTGTGAGGGGATTCACAAATCACTCACGACG	900		
DB	841	AGGTCTCTCAGTTGAGACCAASACCGTGTGAGGGGATTCACAAATCACTCACGACG	900		
QY	901	TGGCCCTTGAGCAACATGAGGAGTGTGCTGTGTGTCAGAGGGAGCACAGGAGTACG	960		
DB	901	TGGCCCTTGAGCAACATGAGGAGTGTGCTGTGTGTCAGAGGGAGCACAGGAGTACG	960		
QY	961	CGCATCACCACAGCAGCTCTTCCAGAGCTGTGTCAGTGTGCTGATTTCTATTAGA	1020		
DB	961	CGCATCACCACAGCAGCTCTTCCAGAGCTGTGTCAGTGTGCTGATTTCTATTAGA	1020		
QY	1021	GAACGTATGGTTATCTCCATCTTAATCTCAGTGTGTTTCAAGGACCTTTTCATCTT	1080		

DB	1021	GAACGTATGGTTATCTCCATCTTAATCTCAGTGTGTTTCTCAGGACCTTTCACTT	1080		
QY	1081	CAGGATTTTACAGTGCATTTCTGAAGAGGAGACATCAACAGAAATTTAGGAGTTGTGCAACA	1140		
DB	1081	CAGGATTTTACAGTGCATTTCTGAAGAGGAGACATCAACAGAAATTTAGGAGTTGTGCAACA	1140		
QY	1141	GCTCTTTTGAGAGAGGCGCTTAAAGGACAGAGAAAGGCTTCAATCGTGAAGAAAT	1200		
DB	1141	GCTCTTTTGAGAGAGGCGCTTAAAGGACAGAGAAAGGCTTCAATCGTGAAGAAAT	1200		
QY	1201	TAAATGTTGTTAAATAGATCACAGCTAGTTTCAAGTTTACCATGTATTCACCT	1260		
DB	1201	TAAATGTTGTTAAATAGATCACAGCTAGTTTCAAGTTTACCATGTATTCACCT	1260		
QY	1261	AGCTGGGTTCTGTATTTTCACTTCTTTCGATACGGCTTATAGGTAATGTCAAGTACAGGAAAA	1320		
DB	1261	AGCTGGGTTCTGTATTTTCACTTCTTTCGATACGGCTTATAGGTAATGTCAAGTACAGGAAAA	1320		
QY	1321	AAACTGTGCAAGTGAGCACCTGATTCGTTGCCCTTAACTCTAAAGCTCCATGCTCT	1380		
DB	1321	AAACTGTGCAAGTGAGCACCTGATTCGTTGCCCTTAACTCTAAAGCTCCATGCTCT	1380		
QY	1381	GGGCTTAAATCGTATTAATCTGATTTTCTGATTTTCTGCTCATATTCACATATG	1440		
DB	1381	GGGCTTAAATCGTATTAATCTGATTTTCTGATTTTCTGCTCATATTCACATATG	1440		
QY	1441	TAAACCAAGACATTTCTATGTACTACAAACCTGTTTAAAAAGGAACTATGTTGCTATG	1500		
DB	1441	TAAACCAAGACATTTCTATGTACTACAAACCTGTTTAAAAAGGAACTATGTTGCTATG	1500		
QY	1501	AATTAACCTTGTGCTGATGCTGATAGGACAGACTGGA	1536		
DB	1501	AATTAACCTTGTGCTGATGCTGATAGGACAGACTGGA	1536		

RESULT 3
US-10-178-442-1
; Sequence 1, Application US/10178442
; Publication No. US20030113870A1
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
; FILE REFERENCE: 11669.112US2
; CURRENT APPLICATION NUMBER: US/10/178,442
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 09/265,686
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: US 09/184,216
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: US 09/040,220
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2825
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2689)..(2689)
; OTHER INFORMATION: Any nucleotide
US-10-178-442-1

Query Match 99.8%; Score 1532.6; DB 14; Length 2825;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 GTAAATTCAGTTTCCAGCAACAGGAAACAGAGTACAGATCTCAGCATGAGA 63
DB 341 GTAAATTCAGTTTCCAGCAACAGGAAACAGAGTACAGATCTCAGCATGAGA 400

QY	64	GAATTTACTGTCTCTACTATGAGGATTTACAGACCCCAAGGTTTCCTCATCTATTC	123
Db	401	GAATTTACTGTCTCTACTATGAGGATTTACAGACCCCAAGGTTTCCTCATCTATTC	460
QY	124	CAAGAAATACGGTCTTGGTATGAGATTTAGTAGCAGTAGAGGAAATGTATGGATCAAC	183
Db	461	CAAGAAATACGGTCTTGGTATGAGATTTAGTAGCAGTAGAGGAAATGTATGGATCAAC	520
QY	184	TTACGTTTGATGAAGATTTGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT	243
Db	521	TTACGTTTGATGAAGATTTGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT	580
QY	244	TTGTAGAGTTGAGGACCCAGGATGAGAACTATATAGGCGCTGGTGGTCTTGGA	303
Db	581	TTGTAGAGTTGAGGACCCAGGATGAGAACTATATAGGCGCTGGTGGTCTTGGA	640
QY	304	CTGTACCAAGGAAACAGATTTCTAAAGGAAATCAAAATAGGATAAGATTTGTATCTGATG	363
Db	641	CTGTACCAAGGAAACAGATTTCTAAAGGAAATCAAAATAGGATAAGATTTGTATCTGATG	700
QY	364	AATATTTTCTTGTACCAAGGTTCTGCATCCACTACACATTTGTATGCCCAATTC	423
Db	701	AATATTTTCTTGTACCAAGGTTCTGCATCCACTACACATTTGTATGCCCAATTC	760
QY	424	CAGAGCTGTGAGTCTTCTAGTGTCTACCCCTTTCAGCTTTGCCACTGACCTGTTAATA	483
Db	761	CAGAGCTGTGAGTCTTCTAGTGTCTACCCCTTTCAGCTTTGCCACTGACCTGTTAATA	820
QY	484	ATGCTATAACTGCCCTTAGTACCTTGGAGAACCTTTATTCGATATCTTGAACCAAGAGAT	543
Db	821	ATGCTATAACTGCCCTTAGTACCTTGGAGAACCTTTATTCGATATCTTGAACCAAGAGAT	880
QY	544	GGCAGTTGGACTTAGAGATCTATATAGCCCACTTGGCAACTTCTTGGCAAGGCTTTTG	603
Db	881	GGCAGTTGGACTTAGAGATCTATATAGCCCACTTGGCAACTTCTTGGCAAGGCTTTTG	940
QY	604	TTTTTGGAGAAATCCAGAGTGTGGATCTGAACCTTTCTAACGAGGAGTAAAGATTAT	663
Db	941	TTTTTGGAGAAATCCAGAGTGTGGATCTGAACCTTTCTAACGAGGAGTAAAGATTAT	1000
QY	664	ACAGTGCACACCTCGTAATCTTCAAGTGTCCATTAAGGAGAACTAAAGAACCGATA	723
Db	1001	ACAGTGCACACCTCGTAATCTTCAAGTGTCCATTAAGGAGAACTAAAGAACCGATA	1060
QY	724	CCATTTTCTGCGCAGGTTGTCTCTGTTTAAACGCTGTGGTGGAACTGTGCTGTGTC	783
Db	1061	CCATTTTCTGCGCAGGTTGTCTCTGTTTAAACGCTGTGGTGGAACTGTGCTGTGTC	1120
QY	784	TCCCAATTTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTTACTAAAAAATACCGAGG	843
Db	1121	TCCCAATTTGCAATGAATGTGTCAATGTGTCCCAAGCAAAAGTTTACTAAAAAATACCGAGG	1180
QY	844	TCCTTCAGTTGAGCAAAACCGGTGTGAGGGATTCACAAATCACTCACCGAGG	903
Db	1181	TCCTTCAGTTGAGCAAAACCGGTGTGAGGGATTCACAAATCACTCACCGAGG	1240
QY	904	CCCTGAGCACCATGAGGAGTGTGATGTGTGTGAGAGGAGCAGAGGAGTATGCCCG	963
Db	1241	CCCTGAGCACCATGAGGAGTGTGATGTGTGTGAGAGGAGCAGAGGAGTATGCCCG	1300
QY	964	ATCACCAACAGCAGCTCTTTGCCAGAGCTGTGAGTGCAGTGGCTGATTTATTAGAA	1023
Db	1301	ATCACCAACAGCAGCTCTTTGCCAGAGCTGTGAGTGCAGTGGCTGATTTATTAGAA	1360
QY	1024	CGTATCGGTATCTCATCTCTTAATCTCAGTGTGTGCTTTCAGGACCTTTCATCTTCAG	1083
Db	1361	CGTATCGGTATCTCATCTCTTAATCTCAGTGTGTGCTTTCAGGACCTTTCATCTTCAG	1420
QY	1084	GATTTTACGTGCAATCTTGAAGAGGAGACATCAAAAGAAATTAAGGAGTTGTGCAACAGCT	1143
Db	1421	GATTTTACGTGCAATCTTGAAGAGGAGACATCAAAAGAAATTAAGGAGTTGTGCAACAGCT	1480
QY	1144	CTTTTGGAGGAGGCGCTTAAAGGACAGGAGAAAGGCTTTCATCTGTTGGAAGAAATTTAA	1203

RESULT 4
US-09-978-295A-487
; Sequence 487, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavich, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13

1 PRIOR APPLICATION NUMBER: 60/066364
2 PRIOR FILING DATE: 1997-11-21
3 PRIOR APPLICATION NUMBER: 60/077450
4 PRIOR FILING DATE: 1998-03-10
5 PRIOR APPLICATION NUMBER: 60/077632
6 PRIOR FILING DATE: 1998-03-11
7 PRIOR APPLICATION NUMBER: 60/077641
8 PRIOR FILING DATE: 1998-03-11
9 PRIOR APPLICATION NUMBER: 60/077649
10 PRIOR FILING DATE: 1998-03-11
11 PRIOR APPLICATION NUMBER: 60/077791
12 PRIOR FILING DATE: 1998-03-12
13 PRIOR APPLICATION NUMBER: 60/078004
14 PRIOR FILING DATE: 1998-03-13
15 PRIOR APPLICATION NUMBER: 60/078886
16 PRIOR FILING DATE: 1998-03-20
17 PRIOR APPLICATION NUMBER: 60/078936
18 PRIOR FILING DATE: 1998-03-20
19 PRIOR APPLICATION NUMBER: 60/078910
20 PRIOR FILING DATE: 1998-03-20
21 PRIOR APPLICATION NUMBER: 60/078939
22 PRIOR FILING DATE: 1998-03-20
23 PRIOR APPLICATION NUMBER: 60/079294
24 PRIOR FILING DATE: 1998-03-25
25 PRIOR APPLICATION NUMBER: 60/079656
26 PRIOR FILING DATE: 1998-03-26
27 PRIOR APPLICATION NUMBER: 60/079664
28 PRIOR FILING DATE: 1998-03-27
29 PRIOR APPLICATION NUMBER: 60/079689
30 PRIOR FILING DATE: 1998-03-27
31 PRIOR APPLICATION NUMBER: 60/079663
32 PRIOR FILING DATE: 1998-03-27
33 PRIOR APPLICATION NUMBER: 60/079728
34 PRIOR FILING DATE: 1998-03-27
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36 PRIOR FILING DATE: 1998-03-27
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40 PRIOR FILING DATE: 1998-03-30
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46 PRIOR FILING DATE: 1998-03-31
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48 PRIOR FILING DATE: 1998-03-31
49 PRIOR APPLICATION NUMBER: 60/080327
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56 PRIOR FILING DATE: 1998-04-01
57 PRIOR APPLICATION NUMBER: 60/081070
58 PRIOR FILING DATE: 1998-04-08
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60 PRIOR FILING DATE: 1998-04-08
61 PRIOR APPLICATION NUMBER: 60/081071
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63 PRIOR APPLICATION NUMBER: 60/081195
64 PRIOR FILING DATE: 1998-04-08
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69 PRIOR APPLICATION NUMBER: 60/081955
70 PRIOR FILING DATE: 1998-04-15
71 PRIOR APPLICATION NUMBER: 60/081817
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73 PRIOR APPLICATION NUMBER: 60/081819

74 PRIOR FILING DATE: 1998-04-15
75 PRIOR APPLICATION NUMBER: 60/081952
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77 PRIOR APPLICATION NUMBER: 60/081838
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95 PRIOR APPLICATION NUMBER: 60/083322
96 PRIOR FILING DATE: 1998-04-28
97 PRIOR APPLICATION NUMBER: 60/083392
98 PRIOR FILING DATE: 1998-04-29
99 PRIOR APPLICATION NUMBER: 60/083495
100 PRIOR FILING DATE: 1998-04-29
101 PRIOR APPLICATION NUMBER: 60/083496
102 PRIOR FILING DATE: 1998-04-29
103 PRIOR APPLICATION NUMBER: 60/083499
104 PRIOR FILING DATE: 1998-04-29
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111 PRIOR APPLICATION NUMBER: 60/083559
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115 PRIOR APPLICATION NUMBER: 60/083742
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122 PRIOR FILING DATE: 1998-05-06
123 PRIOR APPLICATION NUMBER: 60/084637
124 PRIOR FILING DATE: 1998-05-07
125 PRIOR APPLICATION NUMBER: 60/084639
126 PRIOR FILING DATE: 1998-05-07
127 PRIOR APPLICATION NUMBER: 60/084640
128 PRIOR FILING DATE: 1998-05-07
129 PRIOR APPLICATION NUMBER: 60/084598
130 PRIOR FILING DATE: 1998-05-07
131 PRIOR APPLICATION NUMBER: 60/084600
132 PRIOR FILING DATE: 1998-05-07
133 PRIOR APPLICATION NUMBER: 60/084627
134 PRIOR FILING DATE: 1998-05-07
135 PRIOR APPLICATION NUMBER: 60/084643
136 PRIOR FILING DATE: 1998-05-07
137 PRIOR APPLICATION NUMBER: 60/085339
138 PRIOR FILING DATE: 1998-05-13
139 PRIOR APPLICATION NUMBER: 60/085338
140 PRIOR FILING DATE: 1998-05-13
141 PRIOR APPLICATION NUMBER: 60/085323
142 PRIOR FILING DATE: 1998-05-13
143 PRIOR APPLICATION NUMBER: 60/085582
144 PRIOR FILING DATE: 1998-05-15
145 PRIOR APPLICATION NUMBER: 60/085700
146 PRIOR FILING DATE: 1998-05-15

Query Match 99.8%; Score 1532.6; DB 10; Length 2849;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

4 GTAAATTCAGATTTCCAGCAACAAAGAAAGAGAGAGATCAAGATCCTCAGCATGAGA 63
367 GTAAATTCAGATTTCCAGCAACAAAGAAAGAGAGATCAAGATCCTCAGCATGAGA 426

64 GAATATTTACTGCTCTACTAATGAGATTTTCAGCCCAAGGTTTCTCATCTTATC 123
427 GAATATTTACTGCTCTACTAATGAGATTTTCAGCCCAAGGTTTCTCATCTTATC 486

124 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATGTATGGATACAAC 183
487 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATGTATGGATACAAC 546

184 TTAGCTTTGATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
547 TTAGCTTTGATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 606

244 TTGTAGAGATTTGAGAAACCCAGTGTATGAACTATATAGGGCGCTGGTGTCTCGGTA 303
607 TTGTAGAGATTTGAGAAACCCAGTGTATGAACTATATAGGGCGCTGGTGTCTCGGTA 666

304 CTGTACCAAGAAACAGATTTCTAAAGAAATCAAATTAGAGATAGATTTGTATCTGATG 363
667 CTGTACCAAGAAACAGATTTCTAAAGAAATCAAATTAGAGATAGATTTGTATCTGATG 726

364 AATATTTTCTTCTGAAACAGGGTTCTGCATCCACTCAACATTTCTCATGCCAATTCATCA 423
727 AATATTTTCTTCTGAAACAGGGTTCTGCATCCACTCAACATTTCTCATGCCAATTCATCA 786

424 CAGAGCTGTGAGTCTTCTCAGTGTACCCCTTACGCTTGGCACTGACCTGTCTTAATA 483
787 CAGAGCTGTGAGTCTTCTCAGTGTACCCCTTACGCTTGGCACTGACCTGTCTTAATA 846

484 ATGCTATAACCTGCTTTAGTACCTTTGGAGAGCTTATTCGATATCTTGAACAGAGAGAT 543
847 ATGCTATAACCTGCTTTAGTACCTTTGGAGAGCTTATTCGATATCTTGAACAGAGAGAT 906

544 GGCAGTTGGACTTAGAGATCTATATAGCCCACTTGGCACTTCTTGGCAAGGCTTTTG 603
907 GGCAGTTGGACTTAGAGATCTATATAGCCCACTTGGCACTTCTTGGCAAGGCTTTTG 966

604 TTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTTAACAGAGAGGATTAAGATTAT 663
967 TTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTTAACAGAGAGGATTAAGATTAT 1026

664 ACAGCTGCACACTCGTAACTTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACCGATA 723
1027 ACAGCTGCACACTCGTAACTTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACCGATA 1086

724 CCAATTTCTGGCCAGGTTCTCTCGTTTAAAGCTGTGTGGAGCTGTGCTGTGTC 783
1087 CCAATTTCTGGCCAGGTTCTCTCGTTTAAAGCTGTGTGGAGCTGTGCTGTGTC 1146

784 TCCAAATTTGCAATGCAATGTCAATGTGTCCCAAGCAAGTCTTAAATAATACCGAGG 843
1147 TCCAAATTTGCAATGCAATGTCAATGTGTCCCAAGCAAGTCTTAAATAATACCGAGG 1206

844 TCTTCAGTTGAGACCAAAACCGGTGTGAGGGGATTCAGGGGATTCACAAATCACTCAGGAGTGG 903

1207 TCCTTCAGTTGAGACCAAGACCCGGTGTCAAGGATTTGCAAAATCACTCACCACGTGG 1266
904 CCTGGAGACCATGAGGAGTGTGACTGTGTGTGCAGAGGAGACACAGGAGGATAGCGGC 963
1267 CCTGGAGACCATGAGGAGTGTGACTGTGTGTGCAGAGGAGACACAGGAGGATAGCGGC 1326
964 ATCAACACAGAGCTCTTGGCCAGAGCTGTGCAGTGCAGTGGCTGATTTCTATTAGAGAA 1023
1327 ATCAACACAGAGCTCTTGGCCAGAGCTGTGCAGTGCAGTGGCTGATTTCTATTAGAGAA 1386
1024 GGTATGGTTTATCTCCATCTTAATCTCAGTGTGTTTCTCAAGGACCTTTCATCTTCAG 1083
1387 GGTATGGTTTATCTCCATCTTAATCTCAGTGTGTTTCTCAAGGACCTTTCATCTTCAG 1446
1084 GATTTACAGTGCATTTCTGAAAGAGGAGACATCAAAACAGAAATTTAGGAGTTGTGCAACAGCT 1143
1447 GATTTACAGTGCATTTCTGAAAGAGGAGACATCAAAACAGAAATTTAGGAGTTGTGCAACAGCT 1506
1144 CTTTTGAGAGAGGCTTAAAGGACAGGAGAAAGGTCTTCAATCGTGGAAAGAAATTTAA 1203
1507 CTTTTGAGAGAGGCTTAAAGGACAGGAGAAAGGTCTTCAATCGTGGAAAGAAATTTAA 1566
1204 ATGTTGTATTAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTTCCACTAGC 1263
1567 ATGTTGTATTAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTTCCACTAGC 1626
1264 TGGGTTCTGTATTTTCAGTTCCTTCGATACGGCTTAGGGTAAATGTCAGTACAGGAAAAAAA 1323
1627 TGGGTTCTGTATTTTCAGTTCCTTCGATACGGCTTAGGGTAAATGTCAGTACAGGAAAAAAA 1686
1324 CTGTGCAAGTACAGACCTGATTCGGTTCGCTTAACTTAAGTCCATGTCTCTGGG 1383
1687 CTGTGCAAGTACAGACCTGATTCGGTTCGCTTAACTTAAGTCCATGTCTCTGGG 1746
1384 CCTAAATTCGATATAAATCTCGATTTTTTTTTTTTTTTTTTTTTTCTCATATTCATATGTAA 1443
1747 CCTAAATTCGATATAAATCTCGATTTTTTTTTTTTTTTTTTTTTTCTCATATTCATATGTAA 1806
1444 ACCGAAATCTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1503
1807 ACCGAAATCTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1866
1504 TAAACTTGTGCTATGCTCATAGGACAGACTGGA 1536
1867 TAAACTTGTGCTATGCTCATAGGACAGACTGGA 1899

RESULT 5
US-09-978-697-487
; Sequence 487, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
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PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
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PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
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QY	64	GAATTTACTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCCTCATCTTATC	123						
DB	427	GAATTTACTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCCTCATCTTATC	486						
QY	124	CAAGAAATACGCTCTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATCAAC	183						
DB	487	CAAGAAATACGCTCTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATCAAC	546						
QY	184	TTACGTTTGTATGAAGATTGGGCTTGAAGACCAGAGATGACATATGCAAGTATGATT	243						
DB	547	TTACGTTTGTATGAAGATTGGGCTTGAAGACCAGAGATGACATATGCAAGTATGATT	606						
QY	244	TTGTAGAAGTTGAGAACCCAGTGCATGAACTATATTAGGGCGCTGGTGGTTCTGGTA	303						
DB	607	TTGTAGAAGTTGAGAACCCAGTGCATGAACTATATTAGGGCGCTGGTGGTTCTGGTA	666						
QY	304	CTGTACCAGGAAACAGATTTCCTAAGGAAATCAAAATTAGGATAAGATTGTATCTGATG	363						
DB	667	CTGTACCAGGAAACAGATTTCCTAAGGAAATCAAAATTAGGATAAGATTGTATCTGATG	726						
QY	364	AATATTTTCTTCTGAACAGGTTCTGCATCCACTACAAATGTATGATGCCAAATTC	423						
DB	727	AATATTTTCTTCTGAACAGGTTCTGCATCCACTACAAATGTATGATGCCAAATTC	786						
QY	424	CAGAGCTGTGAGTCTTCTGAGTGTACCCCTTCTGAGTTTCCCACTGACCTGCTTAATA	483						
DB	787	CAGAGCTGTGAGTCTTCTGAGTGTACCCCTTCTGAGTTTCCCACTGACCTGCTTAATA	846						
QY	484	ATGCTATAACTGCCTTTAGTACTTGGAGACCTTTATTCGATATCTTGAACACAGAGAT	543						
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QY	664	ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA	723
DB	1027	ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA	1086
QY	724	CAATTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTGGTGGAACTGTCCCTGTGTCT	783
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QY	784	TCCACAATTTGCAATGAATGTCAATGTGCCAAGCAAAAGTTACTAAAAAATATACACGAGG	843
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QY	844	TCCTTCAGTTGAGACCAAAACCGGTTGTGAGGGGATTGCAAAATCATCTCCGACGCTGG	903
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QY	904	CCCTGGAGCCATGAGGAGTGTGACTGTGTGCGAGGGGACACAGGAGGATAGCCGC	963
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APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deanoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerbet, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630Plc3
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; TITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: 60/083742					
PRIOR FILING DATE: 1998-04-30					
PRIOR APPLICATION NUMBER: 60/084366					
PRIOR FILING DATE: 1998-05-05					
PRIOR APPLICATION NUMBER: 60/084414					
PRIOR FILING DATE: 1998-05-06					
PRIOR APPLICATION NUMBER: 60/084441					
PRIOR FILING DATE: 1998-05-06					
PRIOR APPLICATION NUMBER: 60/084637					
PRIOR FILING DATE: 1998-05-07					
PRIOR APPLICATION NUMBER: 60/084639					
PRIOR FILING DATE: 1998-05-07					
PRIOR APPLICATION NUMBER: 60/084640					
PRIOR FILING DATE: 1998-05-07					
PRIOR APPLICATION NUMBER: 60/084598					
PRIOR FILING DATE: 1998-05-07					
PRIOR APPLICATION NUMBER: 60/084600					
PRIOR FILING DATE: 1998-05-07					
PRIOR APPLICATION NUMBER: 60/084627					
PRIOR FILING DATE: 1998-05-07					
PRIOR APPLICATION NUMBER: 60/084643					
PRIOR FILING DATE: 1998-05-07					
PRIOR APPLICATION NUMBER: 60/085339					
PRIOR FILING DATE: 1998-05-13					
PRIOR APPLICATION NUMBER: 60/085338					
PRIOR FILING DATE: 1998-05-13					
PRIOR APPLICATION NUMBER: 60/085323					
PRIOR FILING DATE: 1998-05-13					
PRIOR APPLICATION NUMBER: 60/085582					
PRIOR FILING DATE: 1998-05-15					
PRIOR APPLICATION NUMBER: 60/085700					
PRIOR FILING DATE: 1998-05-15					
PRIOR APPLICATION NUMBER: 60/085689					
PRIOR FILING DATE: 1998-05-15					
PRIOR APPLICATION NUMBER: 60/085579					
PRIOR FILING DATE: 1998-05-15					
PRIOR APPLICATION NUMBER: 60/085580					
PRIOR FILING DATE: 1998-05-15					
PRIOR APPLICATION NUMBER: 60/085573					
PRIOR FILING DATE: 1998-05-15					
PRIOR APPLICATION NUMBER: 60/085704					
PRIOR FILING DATE: 1998-05-15					
PRIOR APPLICATION NUMBER: 60/085697					
Query Match		99.8%; Score 1532.6; DB 10; Length 2849;			

Db 1387 CGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGGCTTCAAGGACCTTTTCATCTTCAG 1446
QY 1084 GATTTACAGTCTGTAAGAGAGGAGACATCAACAGCAATTAGGAGTTGTGCAACAGCT 1143
Db 1447 GATTTACAGTCTGTAAGAGAGGAGACATCAACAGCAATTAGGAGTTGTGCAACAGCT 1506
QY 1144 CTTTGGAGAGGCGCTTAAAGGACAGGAGAAAGGCTCTCAATCGTGGAAAGAAATTTAA 1203
Db 1507 CTTTGGAGAGGAGGCGCTTAAAGGACAGGAGAAAGGCTCTCAATCGTGGAAAGAAATTTAA 1566
QY 1204 ATGTTGTATTAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTTATTCCTAGC 1263
Db 1567 ATGTTGTATTAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTTATTCCTAGC 1626
QY 1264 TGGGTTCTGTATTTCAAGTTCTTTTCGATACGGCTTAGGTTAAATCTCAGTACAGGAAAAAAA 1323
Db 1627 TGGGTTCTGTATTTCAAGTTCTTTTCGATACGGCTTAGGTTAAATCTCAGTACAGGAAAAAAA 1586
QY 1324 CTGTGCAAGTAGACCTGATTCGGTTCCGTTGCTTAACTCTAAAGTCCATGCTCCTGGG 1383
Db 1687 CTGTGCAAGTAGACCTGATTCGGTTCCGTTGCTTAACTCTAAAGTCCATGCTCCTGGG 1746
QY 1384 CCTAAATCGTATAAATCTGGATTTTTTTTTTTTTTTTTTTTTTGGCTCATATTCACATATGTAA 1443
Db 1747 CCTAAATCGTATAAATCTGGATTTTTTTTTTTTTTTTTTTTTTGGCTCATATTCACATATGTAA 1806
QY 1444 ACCAGAACATTTCTATCTACTACAAACCTGGTTTTTAAAAAGGAACATGTTGCTATGAAT 1503
Db 1807 ACCAGAACATTTCTATCTACTACAAACCTGGTTTTTAAAAAGGAACATGTTGCTATGAAT 1866
QY 1504 TAAACTTGTCATGCTGATAGACAGACTGGA 1536
Db 1867 TAAACTTGTCATGCTGATAGACAGACTGGA 1899

RESULT 8

US-09-978-189-487
; Sequence 487, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
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; PRIOR APPLICATION NUMBER: 60/079728
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; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
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; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09

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907	GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTCTGGCAACTCTTTGGCAAGCGCTTTTG	966
604	TTTTTTGGAGAAAATCCAGAGTGGTGGATCTGAACCTTCTTAAACAGAGGAGGTAAAGATTAT	663
967	TTTTTTGGAGAAAATCCAGAGTGGTGGATCTGAACCTTCTTAAACAGAGGAGGTAAAGATTAT	1026
664	ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTTAAGAGAACCGATA	723
1027	ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTTAAGAGAACCGATA	1086
724	CCATTTTCTGGCCAGGTTGTCTCCTCGTGTAAAACGCTGTGTGTGGGAACCTGTGCGCTGTGTC	783
1087	CCATTTTCTGGCCAGGTTGTCTCCTCGTGTAAAACGCTGTGTGTGGGAACCTGTGCGCTGTGTC	1146
784	TCCACAATTGCAATGAATGTCAATGTCTCCAAAGCAAAAGTTACTTAAAAAATACCAAGAGG	843
1147	TCCACAATTGCAATGAATGTCAATGTCTCCAAAGCAAAAGTTACTTAAAAAATACCAAGAGG	1206
844	TCCTTTCAGTTGAGACCAAASACCGGTGTACGGGGATTGCAAAATCACTCACCGACGTGG	903
1207	TCCTTTCAGTTGAGACCAAAGACCGGTGTACGGGGATTGCAAAATCACTCACCGACGTGG	1266
904	CCCTGGAGCACCATGAGAGTGTACATGTGTGTGCAGAGGAGCACAGGAGGATAGCGCG	963
1267	CCCTGGAGCACCATGAGAGTGTACATGTGTGTGCAGAGGAGCACAGGAGGATAGCGCG	1326
964	ATCACCAACGACGCTCTTCCCAGAGCTGTGCAGTGCAGTGGCTGATCTTATTAGAGAA	1023
1327	ATCACCAACGACGCTCTTCCCAGAGCTGTGCAGTGCAGTGGCTGATCTTATTAGAGAA	1386
1024	CGTATGCGTTATCTCCATCTCTTAATCTCAGTTGTTTGCCTTCAAGGACCTTTCATCTTCAG	1083
1387	CGTATGCGTTATCTCCATCTCTTAATCTCAGTTGTTTGCCTTCAAGGACCTTTCATCTTCAG	1446
1084	GAATTCAGTGCATCTCTGAAGGAGGACATCAACAGAAATTAGGAGTGTGTCAACAGCT	1143
1447	GAATTCAGTGCATCTCTGAAGGAGGACATCAACAGAAATTAGGAGTGTGTCAACAGCT	1506
1144	CTTTTGGAGGAGGCGCTTAAAGGACAGAGAAAAGGCTCTTCAATCGTGGAAAGAAAATTAA	1203
1507	CTTTTGGAGGAGGCGCTTAAAGGACAGAGAAAAGGCTCTTCAATCGTGGAAAGAAAATTAA	1566
1204	ATGTTGTATTTAAATAGATCACCACTAGTTTCAGAGTTACATGTACGTTATTCACATAGC	1263
1567	ATGTTGTATTTAAATAGATCACCACTAGTTTCAGAGTTACATGTACGTTATTCACATAGC	1626
1264	TGGGTTCTGTATTTTCAGTTCCTTTCGATACGCTTATAGGTTAATGTCACTACAGGAAAAAA	1323
1627	TGGGTTCTGTATTTTCAGTTCCTTTCGATACGCTTATAGGTTAATGTCACTACAGGAAAAAA	1686
1324	CTGTGCAAGTGAGCACCTGATTCGGTTGCGCTTAACTCTAAAGCTCCATGTCTCTGGG	1383
1687	CTGTGCAAGTGAGCACCTGATTCGGTTGCGCTTAACTCTAAAGCTCCATGTCTCTGGG	1746
1384	CCCTAAAATCGTATAAAATCTGGAATTTTTTTTTTTTTTTTTTTTGGCTCATATTCACATATGTA	1443
1747	CCCTAAAATCGTATAAAATCTGGAATTTTTTTTTTTTTTTTTTTTGGCTCATATTCACATATGTA	1806
1444	ACCAGAACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACCTATGTTGCTATGAAT	1503
1807	ACCAGAACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACCTATGTTGCTATGAAT	1866
1504	TAAACTTTGTGTCATGCTGATAGGACAGACTGGA	1536
1867	TAAACTTTGTGTCATGCTGATAGGACAGACTGGA	1899

RESULT 10

US-09-978-585A-487

; Sequence 487, Application US/09978585A

; Publication No. US20030049633A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

Db 727 AATATTTTCTTGAACACGAGGTTCTGCATCCACTCAACAATGTCATGCGACAATTC A 786
Qy 424 CAGAAGCTGTGAGTCCTTTCAGTGTACCCCTTTCAGCTTTGCACTGGACCTGCTTAATA 483
Db 787 CAGAAGCTGTGAGTCCTTTCAGTGTACCCCTTTCAGCTTTGCACTGGACCTGCTTAATA 846
Qy 484 ATGCTATACTGCTGCTTTAGTACCTTTGGAAGACCTTATTTCGATATCTTGAACAGAGAT 543
Db 847 ATGCTATACTGCTGCTTTAGTACCTTTGGAAGACCTTATTTCGATATCTTGAACAGAGAT 906
Qy 544 GGCAGTTGACCTTGAAGACTTATATAGCCAACTTTCGCAACTTCTTGCAGAGGCTTTTG 603
Db 907 GGCAGTTGACCTTGAAGACTTATATAGCCAACTTTCGCAACTTCTTGCAGAGGCTTTTG 966
Qy 604 TTTTGGAGAAATCCAGAGTGTGATCTGAACTTCTTAACAGAGGAGGTAAATATT 663
Db 967 TTTTGGAGAAATCCAGAGTGTGATCTGAACTTCTTAACAGAGGAGGTAAATATT 1026
Qy 664 ACAGTGCACACCTGTAACCTTCTAGTGTCCATAAGGAGAACTAAAGAACCGATA 723
Db 1027 ACAGTGCACACCTGTAACCTTCTAGTGTCCATAAGGAGAACTAAAGAACCGATA 1086
Qy 724 CCATTTCTGGCCAGGTTGTCTCTGTTTAAACGCTGTGGTGGAACTGTGCTTCTGTC 783
Db 1087 CCATTTCTGGCCAGGTTGTCTCTGTTTAAACGCTGTGGTGGAACTGTGCTTCTGTC 1146
Qy 784 TCCAAATTTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTTACTAAAAAATACCAAGG 843
Db 1147 TCCAAATTTGCAATGAATGTCAATGTGTCCCAAGCAAAAGTTTACTAAAAAATACCAAGG 1206
Qy 844 TCCTTCAGTTCAGACCAAAACCCGTTGTCAGGGATTCGCAAAATCACTCCACGACGTGG 903
Db 1207 TCCTTCAGTTCAGACCAAAACCCGTTGTCAGGGATTCGCAAAATCACTCCACGACGTGG 1266
Qy 904 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGTCAGAGGGAGCACAGGAGATAGCCGC 963
Db 1267 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGTCAGAGGGAGCACAGGAGATAGCCGC 1326
Qy 964 ATCCACACAGAGCTTGTGCCAGAGCTGTGTCAGTGTGAGTGTGATTTATTTAGAA 1023
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Qy 1024 CGTATGCTTATCTCCATCTTAATCTCAGTGTGTTTGTCTCAAGACCTTTTCATCTTCAG 1083
Db 1387 CGTATGCTTATCTCCATCTTAATCTCAGTGTGTTTGTCTCAAGACCTTTTCATCTTCAG 1446
Qy 1084 GATTTACAGTGCATTTCTGAAAGAGGAGACATCAAAACAGAAATAGGAGTTGTGCAACAGCT 1143
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Qy 1444 ACCAGAACATTCATGTACTACAAACCTGGTTTTTAAAAAGGAACATGTGTTGCTATGAAT 1503
Db 1807 ACCAGAACATTCATGTACTACAAACCTGGTTTTTAAAAAGGAACATGTGTTGCTATGAAT 1866

Qy 1504 TAAACTTGTCTATGCTGATAGGACAGACTGGA 1536
Db 1867 TAAACTTGTCTATGCTGATAGGACAGACTGGA 1899
RESULT 11
US-09-978-191A-487
; Sequence 487, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunes, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PLC4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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, PRIOR APPLICATION NUMBER: 60/085580
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085573
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085704
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.8%; Score 1532.6; DB 11; Length 2849;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTAAATTCAGTTTTCCAGCAACAGGAGTACAGATCCTCAGCATGAGA 63

DB 367 GTAAATTCAGTTTTCCAGCAACAGGAGTACAGATCCTCAGCATGAGA 426

QY 64 GAATATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCTATATTC 123

Db 427 GAATTATTACTGTCTACTAATGGAAGTATTACAGACCCCAAGGTTTCTCATACTTATC 486
Qy 124 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGATGGATACAAC 183
Db 487 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGATGGATACAAC 546
Qy 184 TTACGTTTGTATGAAGATTGGGCTTTGAAGACCCAGAAATGACATATGCAAGTATGATT 243
Db 547 TTACGTTTGTATGAAGATTGGGCTTTGAAGACCCAGAAATGACATATGCAAGTATGATT 606
Qy 244 TTGTAGAGTTGAGGACCCAGGTGATGGAACATATATTAGGCGCTGGTGTGTTCTGGTA 303
Db 607 TTGTAGAGTTGAGGACCCAGGTGATGGAACATATATTAGGCGCTGGTGTGTTCTGGTA 666
Qy 304 CTGTACCCAGGAAACAGATTCTTAAAGGAAATCAAAATTAGGATAAGATTGTATCTGATG 363
Db 667 CTGTACCCAGGAAACAGATTCTTAAAGGAAATCAAAATTAGGATAAGATTGTATCTGATG 726
Qy 364 AATATTTTCTTCTGAAACAGGTTCTGCATCCACTACAACATTGTCATGCCAATTTCA 423
Db 727 AATATTTTCTTCTGAAACAGGTTCTGCATCCACTACAACATTGTCATGCCAATTTCA 786
Qy 424 CAGAGCTGTGAGTCTTCTCAGTGTCTACCCCTTTCAGCTTTGCCACTGGACCTGCTTAATA 483
Db 787 CAGAGCTGTGAGTCTTCTCAGTGTCTACCCCTTTCAGCTTTGCCACTGGACCTGCTTAATA 846
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Db 847 ATGCTATAACTGCTTTTAGTACTTGGAGACCTTATTGATATCTTGAACACAGAGAT 906
Qy 544 GGCAGTTGACCTTAGAGATCTATATAGGCCAATTTGGCAACTTCTTGGCAAGGCTTTTG 603
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Qy 604 TTTTGGAGAAATCCAGAGTGTGGATCTGAACCTTCTAAACAGAGGAGTTAAGATTAT 663
Db 967 TTTTGGAGAAATCCAGAGTGTGGATCTGAACCTTCTAAACAGAGGAGTTAAGATTAT 1026
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Db 1087 CCATTTTGGCCAGGTTCTCTCGTTTAAAGCTGTGGTGGAACTGTGCCCTGTGTTC 1146
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Db 1147 TCACAATTTGCAATGAATGTAATGTCCCAAGCAAAAGTTACTAAAAAATACACGAGG 1206
Qy 844 TCCTTCAGTTGAGACCAAAACCCGGTGTCCAGGGGATTGCAAAATCACTCACCGACGTGG 903
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Qy 904 CCTGAGACCATGAGGAGTGACTGTGTGCAGAGGGACACAGGAGGATACCCG 963
Db 1267 CCTGAGACCATGAGGAGTGACTGTGTGCAGAGGGACACAGGAGGATACCCG 1326
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Db 1327 ATCACCAACGACGCTCTTGCCACAGAGCTGTGCAGTGCAGTGCATCTATTAGAGAA 1386
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Db 1387 CGTATCGGTTATCTCATCTTAACTCAGTTGTTTTCATAGGACCTTTTCATCTCAG 1446
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Db 1627 TGGGTTCTGTATTAGTTCTTTTCGATACGGCTTAGGTTAATGTCAGTACAGGAAAAA 1686
Qy 1324 CTGTGCAAGTACAGCACTGATTCGGTTGCTTTAACTCTAAAGCTCCATGTCTCTGGG 1383
Db 1687 CTGTGCAAGTACAGCACTGATTCGGTTGCTTTAACTCTAAAGCTCCATGTCTCTGGG 1746
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Db 1747 CTTAAATCTGTATAAAATCTGGATTTTTTTTTTTTTTGTCTCATATTACATATGTAA 1806
Qy 1444 ACCAGAACATCTATGCTACTACAACTGGTTTAAAGAGGAACATGTTGCTATGAAT 1503
Db 1807 ACCAGAACATCTATGCTACTACAACTGGTTTAAAGAGGAACATGTTGCTATGAAT 1866
Qy 1504 TAAACTTGTGTCTATGCTGATAGACAGACTGGA 1536
Db 1867 TAAACTTGTGTCTATGCTGATAGACAGACTGGA 1899

RESULT 12

US-09-978-403A-487

; Sequence 487, Application US/09978403A

; Publication No. US20030050240A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Baton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C17

; CURRENT APPLICATION NUMBER: US/09/978,403A

; PRIOR FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

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/ PRIOR APPLICATION NUMBER: 60/085579
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 / PRIOR APPLICATION NUMBER: 60/085697

Query Match	99.8%;	Score 1532.6;	DB 11;	Length 2849;
Best Local Similarity	99.9%;	Pred. No. 0;		
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QY	244	TTGTAGAAGTTGAGGA	ACCCAGTGATGGAAT	ATATTAGGCGCTGGTGGTTCTGGTA 303
DB	607	TTGTAGAAGTTGAGGA	ACCCAGTGATGGAAT	ATATTAGGCGCTGGTGGTTCTGGTA 666
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DB	787	CAGAAGCTGTGAGT	CCCTTCAGTGTCACT	ACCCCTTCAGCTTTGCCACTGCACTGCTTAATA 846
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DB	847	ATGCTATAACTGCT	TTTAGTACCTTTGGA	AGACCTTATTCGATATCTTTGAACACGAGAGAT 906
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DB	907	GGCAGTTGGACTTT	AGAAAGTCTATATAG	GCCAACTCTTTGGCAAGGCTTTTG 966
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DB	967	TTTTTGAAGAAAAAT	CCAGAGTGGTGAAT	CTGAACCTTTCTAACAGAGGAGGTAAAGATTAT 1026
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DB	1027	ACAGCTGCACACCT	CGTAACTTCTCAGT	GTCCATAGGGAAGAACTAAAGAAACCGGATA 1086
QY	724	CCATTTTCTGGCC	AGGTTGTCTCCTG	TTAAACGCTGTGGTGGAACTGTGCCCTGTGTGTC 783
DB	1087	CCATTTTCTGGCC	AGGTTGTCTCCTG	TTAAACGCTGTGGTGGAACTGTGCCCTGTGTGTC 1146
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DB	1207	TCCTTCAAGTTGAGA	CCAAAACCCGCTGT	CAGGGGATTTGCAAAATCACTCAACGACGTGG 1266

APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC25
CURRENT APPLICATION NUMBER: US/09/978,564A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Query Match 99.8%; Score 1532.6; DB 11; Length 2849;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 367 GTAAATTCAGTTTCCAGCAACAAGGACAGAGGATACAGATCCCTCAGCATGAGA 426

QY 64 GAATTAATCTGTCTTACTTAATGGAAGTATTCAGCCCAAGGTTTCTCATACTATC 123
DB 427 GAATTAATCTGTCTTACTTAATGGAAGTATTCAGCCCAAGGTTTCTCATACTATC 486

QY 124 CAAGAAATACGTCCTGGTATGAGATAGTAGCAGTAGAGGAAATGATGATGATCAAC 183
DB 487 CAAGAAATACGTCCTGGTATGAGATAGTAGCAGTAGAGGAAATGATGATGATCAAC 546

QY 184 TTACGTTTGTATGAAGAATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
DB 547 TTACGTTTGTATGAAGAATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 606

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DB 607 TTGTAGAAGTTGAGAACCCAGTGATGGAACTATATPAGGGCGCTGGTGGTTCTGGTA 666

QY 304 CTGTACAGAGAAACAGATTTCTAAAGGAAATCAAAATAGGATAAGATTGATCTGATG 363
DB 667 CTGTACAGAGAAACAGATTTCTAAAGGAAATCAAAATAGGATAAGATTGATCTGATG 726

QY 364 AATATTTTCTTCTGAAACAGAGGTTCTGATCCACTACAACTTGTATGATGCAATTC 423
DB 727 AATATTTTCTTCTGAAACAGAGGTTCTGATCCACTACAACTTGTATGATGCAATTC 786

QY 424 CAGAAGCTGTAGTCTTCTAGTCTACCCCTTTCAGCTTTGCACTGGACCTGCTTAATA 483
DB 787 CAGAAGCTGTAGTCTTCTAGTCTACCCCTTTCAGCTTTGCACTGGACCTGCTTAATA 846

QY 484 ATGCTATACTGCTTTAGTCTTACCTTGAAGACCTTATTCATATCTTGAAACAGAGAT 543
DB 847 ATGCTATACTGCTTTAGTCTTACCTTGAAGACCTTATTCATATCTTGAAACAGAGAT 906

QY 544 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTTGGCAACTTCTTGGCAAGGCTTTTG 603
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QY 604 TTTTGGAGAGAAAATCCAGAGTGGTGGATCTGAACCTTTCTAAACAGAGAGGCTTAAGATTAT 663
DB 967 TTTTGGAGAGAAAATCCAGAGTGGTGGATCTGAACCTTTCTAAACAGAGAGGCTTAAGATTAT 1026

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QY 724 CCAATTTTCTGGCCAGGTTGCTCCTCGTTAAACGCTGTGGTGGAACTGTGCCCTGTGTCTC 783
DB 1087 CCAATTTTCTGGCCAGGTTGCTCCTCGTTAAACGCTGTGGTGGAACTGTGCCCTGTGTCTC 1146

QY 784 TCCACAATTCGAATGAATGTCAATGTCTCCCAAGCAAAAGTTTACTTAAAAAATACCACAGG 843
DB 1147 TCCACAATTCGAATGAATGTCAATGTCTCCCAAGCAAAAGTTTACTTAAAAAATACCACAGG 1206

QY 844 TCCTTCAGTTGAGACCAAAASACCGGTGTGTCAGGGGATTCGCAAAATCACTCACCACTGG 903
DB 1207 TCCTTCAGTTGAGACCAAAAGACCGGTGTGTCAGGGGATTCGCAAAATCACTCACCACTGG 1266

QY 904 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGGACACAGGAGGATAGCGGC 963
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QY 1384 CTTAAATCGTATAAAATCTGGAATTTTTTTTTTTTTTTTTTTTTTTTTTGCCTCATATTCACATATGAA 1443
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DB 1807 ACCAGAACCTTCTATCTACTACAAACCTGGTTTTTAAAGGAACTATGTTGCTATGAAT 1866

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DB 1867 TAAACTTGTGTCAATGCTGATAGGACAGACTGGA 1899

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; Sequence 487, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C65
CURRENT APPLICATION NUMBER: US/09/999,833A
CURRENT FILING DATE: 2001-10-24
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64 PRIOR FILING DATE: 1998-05-15
65 PRIOR APPLICATION NUMBER: 60/085573
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67 PRIOR APPLICATION NUMBER: 60/085704
68 PRIOR FILING DATE: 1998-05-15
69 PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.8%; Score 1532.6; DB 11; Length 2849;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 367 GTAATTCAGTTTTCCAGCAACAAGGAACGAGTAGTCAAGATCCTCAGCATGAGA 426
QY 64 GAATTTACTGTGTCTACTAATGAAGTATTCACAGCCCAAGTTTCTCATATTATC 123
DB 427 GAATTTACTGTGTCTACTAATGAAGTATTCACAGCCCAAGTTTCTCATATTATC 486
QY 124 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGATCAAC 183
DB 487 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGATCAAC 546
QY 184 TTACGTTTGTATGAAGATTGCGGCTTGAAGACCCAGAAAGATGACATATGCAAGTATGATT 243
DB 547 TTACGTTTGTATGAAGATTGCGGCTTGAAGACCCAGAAAGATGACATATGCAAGTATGATT 606
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DB 607 TTGTAGAAGTTGAGGAACCCAGTATGGAACATATATTAGGGCGCTGGTTCCTGTTA 666
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DB 667 CTGTACACAGGAAACAGATTTCTAAAGGAATCAAATTAGGATAAGATTTGTATCTGATG 726
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DB 727 AATATTTTCTTCTGAACACAGGTTCTGCATCCACTACAACATTTGTCATGCCACAATTCA 786
QY 424 CAGAAGCTGTGAGTCTTCACTGCTACCCCTTCACTTGGCTTGGCTGAGCTGCTTAATA 483
DB 787 CAGAAGCTGTGAGTCTTCACTGCTACCCCTTCACTTGGCTTGGCTGAGCTGCTTAATA 846
QY 484 ATGCTATAAATGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACACAGAGAT 543
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QY 604 TTTTGGGAAGAAATCCAGAGTGTGGATCTGAACCTTCTAACAGAGAGGTAAATAT 663
DB 967 TTTTGGGAAGAAATCCAGAGTGTGGATCTGAACCTTCTAACAGAGAGGTAAATAT 1026
QY 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGAAGAACTTAAAGAGAACCGATA 723
DB 1027 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGAAGAACTTAAAGAGAACCGATA 1086
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DB 1087 CCATTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGAACTGTGCTGTGTC 1146
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DB 1327 ATCACCAACAGAGCTCTTGGCCAGAGCTGTGAGTGTGAGTGTGATTTATAGANA 1386
QY 1024 CGTATGCGTTATCTCCATCTTAATCTCAGTTGTTTGTCTCAAGACCTTTTCATCTCAG 1083
DB 1387 CGTATGCGTTATCTCCATCTTAATCTCAGTTGTTTGTCTCAAGACCTTTTCATCTCAG 1446

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Db |||||||
Qy 1447 GATTACAGTGCATTCTGAAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACAGCT 1506
Db |||||||
Qy 1144 CTTTGTGAGGAGGCTAAAGGACACAGGAGAAAGGCTTTCATCGTGGAAAGAAATTAA 1203
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Qy 1507 CTTTGTGAGGAGGCTAAAGGACACAGGAGAAAGGCTTTCATCGTGGAAAGAAATTAA 1566
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Qy 1204 ATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGC 1263
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Qy 1567 ATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGC 1626
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a
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APPLICANT: HELSINKI UNIVERSITY LICENSING LTD.						
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,						
TITLE OF INVENTION: THEREFOR, AND USES THEREOF						
FILE REFERENCE: PCT/US99/22669-LUDWIG INST FOR CANCER						
CURRENT APPLICATION NUMBER: PCT/US99/22668						
CURRENT FILING DATE: 1999-09-30						
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EARLIER FILING DATE: 1998-09-30						
EARLIER APPLICATION NUMBER: 60/108,109						
EARLIER FILING DATE: 1998-11-12						
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EARLIER FILING DATE: 1999-05-21						
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EARLIER FILING DATE: 1999-07-15						
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Qy 301 GTACTGTACAGGAAACAGATTTCTAAAGGAAATCAAAATTAGGTAAGATTTGATCTG 360
Db 301 GTACTGTACAGGAAACAGATTTCTAAAGGAAATCAAAATTAGGTAAGATTTGATCTG 360
Qy 361 ATCAATATTTCTCTGAAACAGGGTCTGATCCACCTACCAATTTGTCTGCCCAAT 420
Db 361 ATCAATATTTCTCTGAAACAGGGTCTGATCCACCTACCAATTTGTCTGCCCAAT 420
Qy 421 TCACAGAGCTGTGAGTCTCTTCACTGCTACCCCTTCACTTTCAGCTTTCACCTGACCTCTTA 480
Db 421 TCACAGAGCTGTGAGTCTCTTCACTGCTACCCCTTCACTTTCAGCTTTCACCTGACCTCTTA 480
Qy 481 ATATGCTATACTGCTTGTAGTACCTTGAAGACCTTATTCGATATCTTGAACAGAGA 540
Db 481 ATATGCTATACTGCTTGTAGTACCTTGAAGACCTTATTCGATATCTTGAACAGAGA 540
Qy 541 GATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTTGGCAACTTTCTTGGCAAGCTT 600
Db 541 GATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTTGGCAACTTTCTTGGCAAGCTT 600
Qy 601 TTGTTTTTGAAGAAATCCAGAGTGTGATCTGAACTTCTTAAACAGAGAGGTAAAT 660
Db 601 TTGTTTTTGAAGAAATCCAGAGTGTGATCTGAACTTCTTAAACAGAGAGGTAAAT 660
Qy 661 TATACAGCTGCACACCTCTGTAATCTTCTCAGTGTGCTAAGGGAAGAACTAAAGAGAACCG 720
Db 661 TATACAGCTGCACACCTCTGTAATCTTCTCAGTGTGCTAAGGGAAGAACTAAAGAGAACCG 720
Qy 721 ATACCAATTTCTGGCCAGGTTGTCTCTGTTAAACGCTGTGTGGGAACTGTGCTGTT 780
Db 721 ATACCAATTTCTGGCCAGGTTGTCTCTGTTAAACGCTGTGTGGGAACTGTGCTGTT 780
Qy 781 GTCTCCACAATTCGAATGATGTCATGTCCTCAAGCAAGTATCTAAATAATACACG 840
Db 781 GTCTCCACAATTCGAATGATGTCATGTCCTCAAGCAAGTATCTAAATAATACACG 840
Qy 841 AGTCTCTTCAAGTTGAGACCAAAACCGGTGTCTAGGGGATGTCACAAATCACTCACCAGCG 900
Db 841 AGTCTCTTCAAGTTGAGACCAAAACCGGTGTCTAGGGGATGTCACAAATCACTCACCAGCG 900
Qy 901 TGGCCCTGGAGCACCATGAGGAGTGTGCTGTGTGAGGGGAGGACAGAGGATAGC 960
Db 901 TGGCCCTGGAGCACCATGAGGAGTGTGCTGTGTGAGGGGAGGACAGAGGATAGC 960
Qy 961 CGCATCACACACAGAGCTCTTTCGCCAGAGCTGTGTCAGTGTGCTGATCTATTAGA 1020
Db 961 CGCATCACACACAGAGCTCTTTCGCCAGAGCTGTGTCAGTGTGCTGATCTATTAGA 1020
Qy 1021 GAACGTATGCGTATCTCCATCTTAATCTCAGTGTGTTTGTCTCAAGACCTTTTCATCTT 1080
Db 1021 GAACGTATGCGTATCTCCATCTTAATCTCAGTGTGTTTGTCTCAAGACCTTTTCATCTT 1080

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QY 1081 CAGGATTTACAGTGCATTTCTGAAAGAGGAGACATCAACAGCAATTAGGATTTGTGCAACA 1140
Db 1081 CAGGATTTACAGTGCATTTCTGAAAGAGGAGACATCAACAGCAATTAGGATTTGTGCAACA 1140
QY 1141 GCTCTTTTGAGAGGGGCTTAAGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAT 1200
Db 1141 GCTCTTTTGAGAGGGGCTTAAGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAT 1200
QY 1201 TAAATGTTGTATTAATAGATCACACAGCTAGTTTTCAGAGTTTACCATGTACGTTATCCACT 1260
Db 1201 TAAATGTTGTATTAATAGATCACACAGCTAGTTTTCAGAGTTTACCATGTACGTTATCCACT 1260
QY 1261 AGCTGGGTTCTGTATTTAGTTCTTTTCGATACGGCTTAGGGTAAATGTCACTACAGGAAA 1320
Db 1261 AGCTGGGTTCTGTATTTAGTTCTTTTCGATACGGCTTAGGGTAAATGTCACTACAGGAAA 1320
QY 1321 AAACGTGTCAAGTACGACCTGATTCCTGCTTGCCTTAACTCTAAAGCTCCATGTCT 1380
Db 1321 AAACGTGTCAAGTACGACCTGATTCCTGCTTGCCTTAACTCTAAAGCTCCATGTCTCT 1380
QY 1381 GGGCTTAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1440
Db 1381 GGGCTTAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1440
QY 1441 TAAACGAGCAATCTTATGTACTACAAACCTGGTTTTTAAAGGAACTATGTTGCTATG 1500
Db 1441 TAAACGAGCAATCTTATGTACTACAAACCTGGTTTTTAAAGGAACTATGTTGCTATG 1500
QY 1501 AATTAACCTTGTGTCATGCTGATAGCAGACTGGA 1536
Db 1501 AATTAACCTTGTGTCATGCTGATAGCAGACTGGA 1536

RESULT 3

US-09-410-349A-4
; Sequence 4, Application US/09410349A
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETHSOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; TITLE OF INVENTION: THEREFOR, AND USES THEREOF
; FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
; CURRENT APPLICATION NUMBER: US/09/410,349A
; CURRENT FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-410-349A-4

Query Match 100.0%; Score 1535.6; DB 21; Length 1536;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGTAAATTTCCAGTGTTCAGTAAACAGGACAGAAACGAGTACAAAGATCCTCAGCATG 60
Db 1 CGGGTAAATTTCCAGTGTTCAGTAAACAGGACAGAAACGAGTACAAAGATCCTCAGCATG 60
QY 61 AGAGAAATATTACTGCTGTCTACTAATGGAAGTATTACAGGCCCAAGGTTTCCCTCATACTT 120
Db 61 AGAGAAATATTACTGCTGTCTACTAATGGAAGTATTACAGGCCCAAGGTTTCCCTCATACTT 120
QY 121 ATCCAAAGAAATACCGTCTTGGTATGAGATTTAGTAGCAGTAGAGGAAATATGATGATAC 180
Db 121 ATCCAAAGAAATACCGTCTTGGTATGAGATTTAGTAGCAGTAGAGGAAATATGATGATAC 180
QY 181 AACTTACCTTTGATGAAAGATTTGGGCTTTGAAGACCCAGAGATGACATATCAAGTAGT 240
Db 181 AACTTACCTTTGATGAAAGATTTGGGCTTTGAAGACCCAGAGATGACATATCAAGTAGT 240
QY 241 ATTTTGTAGAAGTTGAGGAAACCCAGTGTATGAAACTATATTAGGGCGCTGGTGTCTG 300
Db 241 ATTTTGTAGAAGTTGAGGAAACCCAGTGTATGAAACTATATTAGGGCGCTGGTGTCTG 300
QY 301 GTACTGTACCAAGGAAACAGATTTCTAAGGAAATCAAAATTAGGATAAGATTTGTATCTG 360
Db 301 GTACTGTACCAAGGAAACAGATTTCTAAGGAAATCAAAATTAGGATAAGATTTGTATCTG 360
QY 361 ATGAATATTTTCTTCTGAAACCCAGGTTTCTGCATCCACTACAAACATTTGTCATGCCACAAT 420
Db 361 ATGAATATTTTCTTCTGAAACCCAGGTTTCTGCATCCACTACAAACATTTGTCATGCCACAAT 420
QY 421 TCACAGAAAGCTGTGAGTCCCTTCAAGTGTACCCCTTCAAGTGTGCTGCTTGA 480
Db 421 TCACAGAAAGCTGTGAGTCCCTTCAAGTGTACCCCTTCAAGTGTGCTGCTTGA 480
QY 481 ATAATGCTATAAATCGCCTTTAGTACCTTGGAGAGACCTTATTCGATATCTTGAACAGAGA 540
Db 481 ATAATGCTATAAATCGCCTTTAGTACCTTGGAGAGACCTTATTCGATATCTTGAACAGAGA 540
QY 541 GATGCGAGTTGGACTTAGAAGATCTATATAGGCAACTTTGGCAACTTTTGGCAAGGCTT 600
Db 541 GATGCGAGTTGGACTTAGAAGATCTATATAGGCAACTTTGGCAACTTTTGGCAAGGCTT 600
QY 601 TTGTTTTTGGAGAAATCCAGAGTGTGGATCTGAACCTTTCTAACAGAGAGGTAAGAT 660
Db 601 TTGTTTTTGGAGAAATCCAGAGTGTGGATCTGAACCTTTCTAACAGAGAGGTAAGAT 660
QY 661 TATACAGCTGCACACCTCGTAACCTTCTCAGTGTCCATAGGGAAGAACTAAGAGAACG 720
Db 661 TATACAGCTGCACACCTCGTAACCTTCTCAGTGTCCATAGGGAAGAACTAAGAGAACG 720
QY 721 ATACCATTTTCTGGCCAGGTTGTCTCCTGTTAAACCGTGTGGTGGAACTGTGCTGTT 780
Db 721 ATACCATTTTCTGGCCAGGTTGTCTCCTGTTAAACCGTGTGGTGGAACTGTGCTGTT 780
QY 781 GTCTCCCAATTTGCAATGAATGTCAATGTGTCCCAAGCAAGTTTACTAAAAATACCAAG 840
Db 781 GTCTCCCAATTTGCAATGAATGTCAATGTGTCCCAAGCAAGTTTACTAAAAATACCAAG 840
QY 841 AGGTCTTTTCAAGTTGAGACCAAAACCGGTGTGAGGGGATTCACAAATCACTACCCAGC 900
Db 841 AGGTCTTTTCAAGTTGAGACCAAAACCGGTGTGAGGGGATTCACAAATCACTACCCAGC 900
QY 901 TGGCCCTTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGATAGC 960
Db 901 TGGCCCTTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGATAGC 960
QY 961 CGCATACCAACAGAGCTCTTCCAGAGCTGTGCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGA 1020
Db 961 CGCATACCAACAGAGCTCTTCCAGAGCTGTGCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGA 1020
QY 1021 GAACGATGCGTTATCTCCATCTTAACTCTCAGTGTGTTGCTTCAAGGACCTTTTCATCTT 1080
Db 1021 GAACGATGCGTTATCTCCATCTTAACTCTCAGTGTGTTGCTTCAAGGACCTTTTCATCTT 1080

QY 1081 CAGGATTTACAGTGCATCTCTGAAGAGGAGACATCAACAGCAATAGGAGTCTGTGCAACA 1140
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 QY 1081 CAGGATTTACAGTGCATCTCTGAAGAGGAGACATCAACAGCAATAGGAGTCTGTGCAACA 1140
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 QY 1141 GCTCTTTTGAGAGGAGGCTTAAAGGACAGAGAGAAAGGTCTTCAATCGTGGAAAGAAAT 1200
 DB |||||
 QY 1201 TAAATGTTGATTAATAATAGATCACAGAGTAGTTTCAGAGTTACCATGTAGTATCCACT 1260
 DB |||||
 QY 1201 TAAATGTTGATTAATAATAGATCACAGAGTAGTTTCAGAGTTACCATGTAGTATCCACT 1260
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 QY 1261 AGCTGGGTTCTGATTTTCAGTTCCTTTCGATACGGCTTAGGTAATGTCAAGTACAGGAAAA 1320
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 QY 1261 AGCTGGGTTCTGATTTTCAGTTCCTTTCGATACGGCTTAGGTAATGTCAAGTACAGGAAAA 1320
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 QY 1321 AAACGTGCAAGTGAGCACCTGATTCGGTTGCGCTTAACTTAAAGTCCCATGTCCT 1380
 DB |||||
 QY 1321 AAACGTGCAAGTGAGCACCTGATTCGGTTGCGCTTAACTTAAAGTCCCATGTCCT 1380
 DB |||||
 QY 1381 GGGCTTAAATCGTATATAAATCTGATTTTTCGATACGGCTTAGGTAATGTCAAGTACAGGAAAA 1440
 DB |||||
 QY 1381 GGGCTTAAATCGTATATAAATCTGATTTTTCGATACGGCTTAGGTAATGTCAAGTACAGGAAAA 1440
 DB |||||
 QY 1441 TAAACCGAACAATCTATGTACTACAAACCTGGTTTTTAAAGGAACTATGTTGCTATG 1500
 DB |||||
 QY 1441 TAAACCGAACAATCTATGTACTACAAACCTGGTTTTTAAAGGAACTATGTTGCTATG 1500
 DB |||||
 QY 1501 AATTAACCTGTGTCATGCTGATAGGACAGACTGGA 1536
 DB |||||
 QY 1501 AATTAACCTGTGTCATGCTGATAGGACAGACTGGA 1536
 DB |||||

RESULT 4

US-09-852-209-4

; Sequence 4, Application US/09852209

; GENERAL INFORMATION:

; APPLICANT: ERIKSSON, Ulf

; APPLICANT: AASE, Karin

; APPLICANT: LEE, Xuri

; APPLICANT: PONTEN, Annica

; APPLICANT: UUTELA, Marko

; APPLICANT: ALITALO, Kari

; APPLICANT: OESTMAN, Arne

; APPLICANT: HELDIN, Carl-Henrik

; APPLICANT: BEYSHOUTZ, Christer

; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING

; TITLE OF INVENTION: THEREFOR, AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/09/852,209

; CURRENT FILING DATE: 2001-05-10

; PRIOR APPLICATION NUMBER: 09/410,349

; PRIOR FILING DATE: 1999-09-30

; PRIOR APPLICATION NUMBER: 60/110,749

; PRIOR FILING DATE: 1998-12-03

; PRIOR APPLICATION NUMBER: 60/113,002

; PRIOR FILING DATE: 1998-12-18

; PRIOR APPLICATION NUMBER: 60/135,426

; PRIOR FILING DATE: 1999-05-21

; PRIOR APPLICATION NUMBER: 60/144,022

; PRIOR FILING DATE: 1999-07-15

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 1536

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-852-209-4

Query Match

Best Local Similarity

Matches 1536; Conservative

100.08; Score 1535.6; DB 35; Length 1536;

100.08; Pred. No. 0;

Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGTAAATTTCCAGTCTTTCCAGCAACACAGGAACAGACGAGTACAAAGATCCTCAGCATG 60
 DB |||||
 QY 1 CGGGTAAATTTCCAGTCTTTCCAGCAACACAGGAACAGACGAGTACAAAGATCCTCAGCATG 60
 DB |||||
 QY 61 AGAGAATTAATTAATCTGTGTCTACTAATGGAAGTAATTCACAGCCCAAGGTTTCTCATACTT 120
 DB |||||
 QY 61 AGAGAATTAATTAATCTGTGTCTACTAATGGAAGTAATTCACAGCCCAAGGTTTCTCATACTT 120
 DB |||||
 QY 121 ATCCAGAATTAATGAGTCTGTGTATGGAGTTAGTACAGTACAGGAATGATGATGATAC 180
 DB |||||
 QY 121 ATCCAGAATTAATGAGTCTGTGTATGGAGTTAGTACAGTACAGGAATGATGATGATAC 180
 DB |||||
 QY 181 AACTTACGTTTGCATGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATG 240
 DB |||||
 QY 181 AACTTACGTTTGCATGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATG 240
 DB |||||
 QY 241 ATTTGTAGAAATGAGGAAACCCAGTGTAGGAACTATATAGGGCGCTGGTGTGTTCTG 300
 DB |||||
 QY 241 ATTTGTAGAAATGAGGAAACCCAGTGTAGGAACTATATAGGGCGCTGGTGTGTTCTG 300
 DB |||||
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 DB |||||
 QY 301 GTACTGTACCGAAGAAACAGATTTCTTAAAGGAAATCAAAATTAGGATAAGATTTGATCTG 360
 DB |||||
 QY 361 ATGAATTAATTTCTTCTGAAACAGGCTTCTGCATCCACTTCAACATTTGTCATGCCACAAT 420
 DB |||||
 QY 361 ATGAATTAATTTCTTCTGAAACAGGCTTCTGCATCCACTTCAACATTTGTCATGCCACAAT 420
 DB |||||
 QY 421 TCACAGAAGCTGTGAGTCTTCAAGTGTACCCGCTTTCAGCTTTGCGACTTGGCACTGGACCTGCTTA 480
 DB |||||
 QY 421 TCACAGAAGCTGTGAGTCTTCAAGTGTACCCGCTTTCAGCTTTGCGACTTGGCACTGGACCTGCTTA 480
 DB |||||
 QY 481 ATAATGCTATACTGCTCTTTAGTACCTTGGAAAGACCTTATTCGATATCTTGAACACAGAGA 540
 DB |||||
 QY 481 ATAATGCTATACTGCTCTTTAGTACCTTGGAAAGACCTTATTCGATATCTTGAACACAGAGA 540
 DB |||||
 QY 541 GATGGCAGTTGGACTTAGAAGATCTATATAGGCAACTTTGGCAACTTTCTTGGCAAGGCTT 600
 DB |||||
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 QY 601 TTGTTTTTGGAGAAATCCAGAGTGGTGGATCTGAACTTCTAAAGAGGAGGTAAGAT 660
 DB |||||
 QY 661 TATACAGCTGCACACCTCTGTAATCTTCTAGTGTCCATAAGGAAGAACTTAAAGAGAACCG 720
 DB |||||
 QY 661 TATACAGCTGCACACCTCTGTAATCTTCTAGTGTCCATAAGGAAGAACTTAAAGAGAACCG 720
 DB |||||
 QY 721 ATACCAATTTCTGGCCAGGTTGCTCTGTTTAAAGCTTGGTGGAACTGTGCTGTT 780
 DB |||||
 QY 721 ATACCAATTTCTGGCCAGGTTGCTCTGTTTAAAGCTTGGTGGAACTGTGCTGTT 780
 DB |||||
 QY 781 GTCTCCCAATTTGCAATGATGTCATGTCCTTCCAGCAAGTACTTAAATAATACACAG 840
 DB |||||
 QY 781 GTCTCCCAATTTGCAATGATGTCATGTCCTTCCAGCAAGTACTTAAATAATACACAG 840
 DB |||||
 QY 841 AGGTCTCTCAGTTGAGACCAAAACCGGTGTGAGGGGATTCACAAATCACTCACCGACG 900
 DB |||||
 QY 841 AGGTCTCTCAGTTGAGACCAAAACCGGTGTGAGGGGATTCACAAATCACTCACCGACG 900
 DB |||||
 QY 901 TGGCCCTTGGAGCACCATGAGGAGTGTGCTGTGTCAGAGGGAGGACACAGGAGATAGC 960
 DB |||||
 QY 901 TGGCCCTTGGAGCACCATGAGGAGTGTGCTGTGTCAGAGGGAGGACACAGGAGATAGC 960
 DB |||||
 QY 961 CGCATCAACCCAGCAGCTCTTGGCCAGAGCTGTGCGAGTGCAGTGCCTGATTTCTATTAGA 1020
 DB |||||
 QY 961 CGCATCAACCCAGCAGCTCTTGGCCAGAGCTGTGCGAGTGCAGTGCCTGATTTCTATTAGA 1020
 DB |||||
 QY 1021 GAACGATGCGTTATCTCCATCTCTTAACTCAGTTGTTGCTTCAAGGACCTTCTCATCTT 1080
 DB |||||
 QY 1021 GAACGATGCGTTATCTCCATCTCTTAACTCAGTTGTTGCTTCAAGGACCTTCTCATCTT 1080
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 QY 1081 CAGGATTTACAGTGCATTTCTGAAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACA 1140
 DB |||||


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Db 1081 CAGGATTTACAGTGCATTTCTGAAAGAGGAGACATCAAAACAGAAATTTAGGAGTTGTGCAACA 1140
Qy 1141 GCTCTTTTGAGAGAGGCGCTAAAGACAGAGGAGAAAGGCTTCAATCGTGGAGAGAAAT 1200
Db 1141 GCTCTTTTGAGAGAGGCGCTAAAGACAGAGGAGAAAGGCTTCAATCGTGGAGAGAAAT 1200
Qy 1201 TAAATGTTGTAATAATAGATCACAGCTAGTTTCAGAGTTTACCAGTGTACCGTATTTCCACT 1260
Db 1201 TAAATGTTGTAATAATAGATCACAGCTAGTTTCAGAGTTTACCAGTGTACCGTATTTCCACT 1260
Qy 1261 AGCTGGGTTCTGATTTTCAGTTCCTTTCGATACGGCTTAGGGTAATGTCAAGTACAGGAAAA 1320
Db 1261 AGCTGGGTTCTGATTTTCAGTTCCTTTCGATACGGCTTAGGGTAATGTCAAGTACAGGAAAA 1320
Qy 1321 AAACTGTGCAAGTGTGATTCGCTTCCCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCT 1380
Db 1321 AAACTGTGCAAGTGTGATTCGCTTCCCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCT 1380
Qy 1381 GGGCTAAATCGTATATAAATCTGGATTTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCT 1440
Db 1381 GGGCTAAATCGTATATAAATCTGGATTTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCT 1440
Qy 1441 TAAACAGAAATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1500
Db 1441 TAAACAGAAATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1500
Qy 1501 AATTAAACTTGTGTCATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 1536
Db 1501 AATTAAACTTGTGTCATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 1536

RESULT 7
US-10-303-997B-4
; Sequence 4, Application US/10303997B
; GENERAL INFORMATION:
; APPLICANT: LI, Xuri
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: CARMELIET, Peter
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND ANGIOGEN
; FILE REFERENCE: 029065.44740C3
; CURRENT APPLICATION NUMBER: US/10/303,997B
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 60/102,461
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: US 60/108,109
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: US 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: US 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-997B-4

Query Match 100.0%; Score 1535.6; DB 50; Length 1536;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGTAAATTCAGTTCCTGAAACAGGAGACATCAAAACAGAAATTTAGGAGTTGTGCAACA 1140
Db 1 CGGGTAAATTCAGTTCCTGAAAGAGGAGACATCAAAACAGAAATTTAGGAGTTGTGCAACA 1140
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Db 61 AGAGAAATTTACTGCTGTCTACTAATGCAAGTATTTCACAGCCCAAGGTTTCTCTCACTTT 120
Qy 121 ATCCAAGAAATACCGGTCTTGGTATGGAGATTAGTAGCAGTAGTAGAGAAATGTATGGATAC 180
Db 121 ATCCAAGAAATACCGGTCTTGGTATGGAGATTAGTAGCAGTAGTAGAGAAATGTATGGATAC 180
Qy 181 AACTTACGTTTGTATGAAGAATTTGGGCTTGAAGACCCAGAACCCAGAGATGACATATGCAAGTATG 240
Db 181 AACTTACGTTTGTATGAAGAATTTGGGCTTGAAGACCCAGAACCCAGAGATGACATATGCAAGTATG 240
Qy 241 ATTTTGTAGAGTTGAGGAAACCCAGTGTGAACTATATATTAGGGCGCTGGTGGTCTG 300
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Qy 301 GTACTGTACCAAGGAAACAGATTTCTAAAGAAATCAAAATTTAGGATAAGATTTGTATCTG 360
Db 301 GTACTGTACCAAGGAAACAGATTTCTAAAGAAATCAAAATTTAGGATAAGATTTGTATCTG 360
Qy 361 ATGAATATTTTCTTCTGAACAGGGTTCTGCATCCACTACAACTGTCATGCCAAT 420
Db 361 ATGAATATTTTCTTCTGAACAGGGTTCTGCATCCACTACAACTGTCATGCCAAT 420
Qy 421 TCACAGAGCTGTGAGTCCCTTCACTGCTACCCCTTCACTGCTTCCACTGACCTGCTTA 480
Db 421 TCACAGAGCTGTGAGTCCCTTCACTGCTACCCCTTCACTGCTTCCACTGACCTGCTTA 480
Qy 481 AATAATGCTATAACTGCTTCTAGTACCTTGAAGACCTTATTCGATATCTTGAACACAGAGA 540
Db 481 AATAATGCTATAACTGCTTCTAGTACCTTGAAGACCTTATTCGATATCTTGAACACAGAGA 540
Qy 541 GATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAAACCTTCTTGGCAAGGCTT 600
Db 541 GATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAAACCTTCTTGGCAAGGCTT 600
Qy 601 TTGTTTTTGAAGAAATCCAGAGTGTGGATCTGAACTTCTTAACAGAGGAGGTAGAT 660
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Qy 661 TATACAGCTGCACACCTCGTAACTTCTCAGTGTGCATTAAGGAGAACTAAAGAGAACCG 720
Db 661 TATACAGCTGCACACCTCGTAACTTCTCAGTGTGCATTAAGGAGAACTAAAGAGAACCG 720
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Qy 1081 CAGGATTTACAGTGCATTTCTGAAAGAGGAGACATCAAAACAGAAATTTAGGAGTTGTGCAACA 1140
Db 1081 CAGGATTTACAGTGCATTTCTGAAAGAGGAGACATCAAAACAGAAATTTAGGAGTTGTGCAACA 1140
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QY 1141 GCTCTTTTGAGAGAGGCGCTTAAAGACAGAGAAAGGCTCTCAATCGTGGAAAGAAAT 1200
 Db 1141 GCTCTTTTGAGAGAGGCGCTTAAAGACAGAGAAAGGCTCTCAATCGTGGAAAGAAAT 1200
 QY 1201 TAAATGTTGATTAATAAGATACACAGCTAGTTTTCAGAGTTACCATGTAGTATCCACT 1260
 Db 1201 TAAATGTTGATTAATAAGATACACAGCTAGTTTTCAGAGTTACCATGTAGTATCCACT 1260
 QY 1261 AGCTGGGTTCTGATTTTCTGATACCGCTTACCGCTTACCGCTTACCGCTTACCGCT 1320
 Db 1261 AGCTGGGTTCTGATTTTCTGATACCGCTTACCGCTTACCGCTTACCGCTTACCGCT 1320
 QY 1321 AAACCTGCGAAGTGAGCAGCCTGATTCGCTTGCCTTAACTTAACTTAACTTAACTT 1380
 Db 1321 AAACCTGCGAAGTGAGCAGCCTGATTCGCTTGCCTTAACTTAACTTAACTTAACTT 1380
 QY 1381 GGGCTTAAATCGTATATAATCTGATTTTCTGATTTTCTGATTTTCTGATTTTCTGAT 1440
 Db 1381 GGGCTTAAATCGTATATAATCTGATTTTCTGATTTTCTGATTTTCTGATTTTCTGAT 1440
 QY 1441 TAAACCGAAGCATCTATGATCTACCAACCTGGTTTAAAGAGGAACATGTTGCTATG 1500
 Db 1441 TAAACCGAAGCATCTATGATCTACCAACCTGGTTTAAAGAGGAACATGTTGCTATG 1500
 QY 1501 AATTAACCTTGTGTCATCTGATAGGACAGACTGGA 1536
 Db 1501 AATTAACCTTGTGTCATCTGATAGGACAGACTGGA 1536

RESULT 8

US-09-184-216-1
 ; Sequence 1, Application US/09184216
 ; GENERAL INFORMATION:
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Kuo, Sophia S.
 ; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
 ; FILE REFERENCE: P1122P1
 ; CURRENT APPLICATION NUMBER: US/09/184,216
 ; CURRENT FILING DATE: 1998-11-02
 ; NUMBER OF SEQ ID NOS: 8
 ; SEQ ID NO 1
 ; LENGTH: 2825
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: Unknown
 ; LOCATION: 2689
 ; OTHER INFORMATION: Any nucleotide

US-09-184-216-1

Query Match 99.8%; Score 1532.6; DB 16; Length 2825;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GTAAATCCAGTTTCCAGCAACAGGAAACAGACGGAGTCAAGATCCTCAGCATGAGA 63
 Db 341 GTAAATCCAGTTTCCAGCAACAGGAAACAGACGGAGTCAAGATCCTCAGCATGAGA 400
 QY 64 GAATTTACTGTGCTACTAATGGAAGTATTCACGCCAAGGTTTCCCTCATCTTATC 123
 Db 401 GAATTTACTGTGCTACTAATGGAAGTATTCACGCCAAGGTTTCCCTCATCTTATC 460
 QY 124 CAAGAAATACCGTCTTGTGATGGAGTTAGTAGCAGTAGAGGAAATGATGGATACAC 183
 Db 461 CAAGAAATACCGTCTTGTGATGGAGTTAGTAGCAGTAGAGGAAATGATGGATACAC 520
 QY 184 TTACGTTTGAAGAAATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGAT 243
 Db 521 TTACGTTTGAAGAAATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGAT 580
 QY 244 TTGTAGAAAGTTGAGAAACCCAGTATGGAACATATATTAAGGCGCTGGTGTGGTCTG 303
 Db 581 TTGTAGAAAGTTGAGAAACCCAGTATGGAACATATATTAAGGCGCTGGTGTGGTCTG 640

QY 304 CTGTACCAAGGAAACAGATTTTCTAAGGAAATCAAAATTAGGATAGATTGTGTATCTGATG 363
 Db 641 CTGTACCAAGGAAACAGATTTTCTAAGGAAATCAAAATTAGGATAGATTGTGTATCTGATG 700
 QY 364 AATATTTTCTTCTGAAACAGGTTTCTGCATCCACTCAACAATTCATGCGCACAAATTC 423
 Db 701 AATATTTTCTTCTGAAACAGGTTTCTGCATCCACTCAACAATTCATGCGCACAAATTC 760
 QY 424 CAGAAAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTCGCCACTGACCTGCTTAATA 483
 Db 761 CAGAAAGCTGTGAGTCTTTCAGTGTCTACCCCTTTCAGCTTTCGCCACTGACCTGCTTAATA 820
 QY 484 ATGCTTATAACTGCCCTTTAGTACCTTTGGAAGACCTTTATTCGATATCTTGAACACAGAGAGAT 543
 Db 821 ATGCTTATAACTGCCCTTTAGTACCTTTGGAAGACCTTTATTCGATATCTTGAACACAGAGAGAT 880
 QY 544 GGCAGTTGAGCTTTAGAAAGATCTATATAGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG 603
 Db 881 GGCAGTTGAGCTTTAGAAAGATCTATATAGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG 940
 QY 604 TTTTGGAAAGAAATCCAGAGTGGTGGATCTCAACCTTCTAACAGAGAGAGTAAAGATTAT 663
 Db 941 TTTTGGAAAGAAATCCAGAGTGGTGGATCTCAACCTTCTAACAGAGAGAGTAAAGATTAT 1000
 QY 664 ACAGCTGCAACACTCGTAACTTCTCAGTGTCCATAGGGAAGAACTAAAGAAACCGATA 723
 Db 1001 ACAGCTGCAACACTCGTAACTTCTCAGTGTCCATAGGGAAGAACTAAAGAAACCGATA 1060
 QY 724 CCATTTTCTGGCCAGGTTGTCTCTGTTAAACGGTGTGGTGGAACTGTGCTCTGTGTC 783
 Db 1061 CCATTTTCTGGCCAGGTTGTCTCTGTTAAACGGTGTGGTGGAACTGTGCTCTGTGTC 1120
 QY 784 TCCACAAATTCGAATGATGATCAATGTCTCCCAAGCAAACTTACTAAAAATACCCAGAG 843
 Db 1121 TCCACAAATTCGAATGATGATCAATGTCTCCCAAGCAAACTTACTAAAAATACCCAGAG 1180
 QY 844 TCCTTCAGTTTGAGACCAAAASACGGTGTTCAGGGGATTCACAAATCACTCACCAGGTGG 903
 Db 1181 TCCTTCAGTTTGAGACCAAAAGACGGTGTTCAGGGGATTCACAAATCACTCACCAGGTGG 1240
 QY 904 CCTGGAGCACCATGAGGAGTGTGCTGTGTGAGAGGGAGACAGAGAGATAGCCGC 963
 Db 1241 CCTGGAGCACCATGAGGAGTGTGCTGTGTGAGAGGGAGACAGAGAGATAGCCGC 1300
 QY 964 ATCACCACAGCAGCTCTTCCCGCAGAGCTGTGCGAGTGCAGTGGCTGATTTCTATTAGAGAA 1023
 Db 1301 ATCACCACAGCAGCTCTTCCCGCAGAGCTGTGCGAGTGCAGTGGCTGATTTCTATTAGAGAA 1360
 QY 1024 CGTATCGGTTATCTCCATCTTAATCTCAGTTGTGTTGCTTCAAGGACCTTTCTATCTTCAG 1083
 Db 1361 CGTATCGGTTATCTCCATCTTAATCTCAGTTGTGTTGCTTCAAGGACCTTTCTATCTTCAG 1420
 QY 1084 GATTTACAGTGCATCTCTGAAAGAGGAGACATCAAAACGAATTAGGAGTTGTGCAACAGCT 1143
 Db 1421 GATTTACAGTGCATCTCTGAAAGAGGAGACATCAAAACGAATTAGGAGTTGTGCAACAGCT 1480
 QY 1144 CTTTTCAGAGGAGGCTTAAAGGACAGGAGAAAGGCTTCCTCAATCGTGGGAAAGAAATTA 1203
 Db 1481 CTTTTCAGAGGAGGCTTAAAGGACAGGAGAAAGGCTTCCTCAATCGTGGGAAAGAAATTA 1540
 QY 1204 ATGCTGTATTAAATAGATCACCGCTAGTTTTCAGAGTTTACCATGTACGTTATTCCTAGC 1263
 Db 1541 ATGCTGTATTAAATAGATCACCGCTAGTTTTCAGAGTTTACCATGTACGTTATTCCTAGC 1600
 QY 1264 TGGGTTCTGTATTTCAGTTCTTTTCGATACGGCTTAGGGTAAATGTTCAGTACAGGAAAAA 1323
 Db 1601 TGGGTTCTGTATTTCAGTTCTTTTCGATACGGCTTAGGGTAAATGTTCAGTACAGGAAAAA 1660
 QY 1324 CTGTGCAAGTGTAGCACCTGATTCGGTTCCTTAACTCTAAAGCTCCATGTCTCTGGG 1383
 Db 1661 CTGTGCAAGTGTAGCACCTGATTCGGTTCCTTAACTCTAAAGCTCCATGTCTCTGGG 1720

QY 1384 CCTAAATCGTATATAAATCTGGATTTTTTTTTTTTTTTTTTTTTTTTGGCTCATATTCACATATGTAA 1443
Db 1721 CCTAAATCGTATATAAATCTGGATTTTTTTTTTTTTTTTTTTTTTTGGCTCATATTCACATATGTAA 1780
QY 1444 ACCGACATCTATGATCTACAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGAAT 1503
Db 1781 ACCGACATCTATGATCTACAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGAAT 1840
QY 1504 TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1536
Db 1841 TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1873

RESULT 9
US-09-723-749-1
; Sequence 1, Application US/09723749
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
; FILE REFERENCE: P1122P2D1
; CURRENT APPLICATION NUMBER: US/09/723,749
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: US 09/265,686
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: US 09/040,220
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: US 09/184,216
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 1
; LENGTH: 2825
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: Unknown
; LOCATION: 2689
; OTHER INFORMATION: Any nucleotide
US-09-723-749-1

Query Match 99.8%; Score 1532.6; DB 32; Length 2825;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTAATTCAGTTTTCCAGCAACAGGACGAGTACAGATCCTCAGCATGAGA 63
Db 341 GTAATTCAGTTTTCCAGCAACAGGACGAGTACAGATCCTCAGCATGAGA 400
QY 64 GAATTTACTGTCTACTAATGAGTATTCACAGCCAGGTTTCTCATCTTATC 123
Db 401 GAATTTACTGTCTACTAATGAGTATTCACAGCCAGGTTTCTCATCTTATC 460
QY 124 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAAC 183
Db 461 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAAC 520
QY 184 TTACGTTTGATCAAGATTTGGCTTGAACCCAGAGATGACATATGCAAGTATGATT 243
Db 521 TTACGTTTGATCAAGATTTGGCTTGAACCCAGAGATGACATATGCAAGTATGATT 580
QY 244 TTGTAGAAGTTGAGGAAACCCAGTGTGAACTATATTAGGGCGCTGGTGTCTGGTA 303
Db 581 TTGTAGAAGTTGAGGAAACCCAGTGTGAACTATATTAGGGCGCTGGTGTCTGGTA 640
QY 304 CTGTACAGGAAACAGATTTCTAAAGGAATCAAAATAGGATAGATTTGTATCTGATG 363
Db 641 CTGTACAGGAAACAGATTTCTAAAGGAATCAAAATAGGATAGATTTGTATCTGATG 700
QY 364 AATATTTTCTCTGAAACAGGTTTCTGCATCCACTACAACATTTGTCTATGCAATCA 423
Db 701 AATATTTTCTCTGAAACAGGTTTCTGCATCCACTACAACATTTGTCTATGCAATCA 760
QY 424 CAGAAGCTGTAGTCTTCAGTGTCTACCCCTTTCAGCTTTGCCACTGGACCTGCTTAATA 483

Db 761 CAGAAGCTGTAGTCTTCAGTGTCTACCCCTTTCAGCTTTGCCACTGGACCTGCTTAATA 820
QY 484 ATGCTATAACTGCCCTTTAGTACCTTTGGAAGACCTTTATTCGATATCTTGAACAGAGAGAT 543
Db 821 ATGCTATAACTGCCCTTTAGTACCTTTGGAAGACCTTTATTCGATATCTTGAACAGAGAGAT 880
QY 544 GGCAGTTGACATTAAGAGATCTATATAGGCGCACTTGGCAACTCTTGGCAGGCTTTTG 603
Db 881 GGCAGTTGACATTAAGAGATCTATATAGGCGCACTTGGCAACTCTTGGCAGGCTTTTG 940
QY 604 TTTTGGAAAGAAATCCAGAGTGGTGGATCTGAACTTCTTAACAGAGAGGTAAGATTAT 663
Db 941 TTTTGGAAAGAAATCCAGAGTGGTGGATCTGAACTTCTTAACAGAGAGGTAAGATTAT 1000
QY 664 ACAGCTGCAACCTCTGTAACTCTCAGTGTCTAATAGGGAAGAACTAAAGAAACCGATA 723
Db 1001 ACAGCTGCAACCTCTGTAACTCTCAGTGTCTAATAGGGAAGAACTAAAGAAACCGATA 1060
QY 724 CCATTTTCTGGCCAGGTTGCTCTCTGTTAAACGCTGTGGTGGAACTGTGCTGTGTTC 783
Db 1061 CCATTTTCTGGCCAGGTTGCTCTCTGTTAAACGCTGTGGTGGAACTGTGCTGTGTTC 1120
QY 784 TCCACAATTTGCAATGAATGTCAATGTCTCCCAAGCAAAAGTTTACTAAAAATACCAAGAG 843
Db 1121 TCCACAATTTGCAATGAATGTCAATGTCTCCCAAGCAAAAGTTTACTAAAAATACCAAGAG 1180
QY 844 TCCCTCAGTTGAGACCAAAASACGGTGTCCAGGGATTCACAAATCACTCACCGAGCTGG 903
Db 1181 TCCCTCAGTTGAGACCAAAASACGGTGTCCAGGGATTCACAAATCACTCACCGAGCTGG 1240
QY 904 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCAAGAGAGATAGCCGC 963
Db 1241 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCAAGAGAGATAGCCGC 1300
QY 964 ATCAACACAGAGAGCTTTGCCAGAGCTGTGCGAGTGTGCGTGTGCTTATTTAGAGAA 1023
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QY 1024 CGTATGCTTATCTCCATCTTAATCTCAGTTGTGTTTGTCTTCAAGGACCTTTTATCTTCAG 1083
Db 1361 CGTATGCTTATCTCCATCTTAATCTCAGTTGTGTTTGTCTTCAAGGACCTTTTATCTTCAG 1420
QY 1084 GATTTACAGTGTCTGAAAGAGGAGACATCAAAACAGAAATTAGAGTGTGCAACAGCT 1143
Db 1421 GATTTACAGTGTCTGAAAGAGGAGACATCAAAACAGAAATTAGAGTGTGCAACAGCT 1480
QY 1144 CTTTTCAGAGGAGGCTTAAAGGACAGGAAAGGCTTCAATCGTGGAAAGAAATTA 1203
Db 1481 CTTTTCAGAGGAGGCTTAAAGGACAGGAAAGGCTTCAATCGTGGAAAGAAATTA 1540
QY 1204 ATGTTGTATTAAATAGATCACAGCTAGTTTCAGAGTTTACCATTACGTATTTCCACTAGC 1263
Db 1541 ATGTTGTATTAAATAGATCACAGCTAGTTTCAGAGTTTACCATTACGTATTTCCACTAGC 1600
QY 1264 TGGGTTCTGTATTTAGTTTCTGATACGGCTTAGGGTAATGTCTAGTACAGGAAATAA 1323
Db 1601 TGGGTTCTGTATTTAGTTTCTGATACGGCTTAGGGTAATGTCTAGTACAGGAAATAA 1660
QY 1324 CTGTCAAGTGTAGCACCTGATTCCTGCTTGGCTTTAACTCTAAAGCTCCATGTCTCTGGG 1383
Db 1661 CTGTCAAGTGTAGCACCTGATTCCTGCTTGGCTTTAACTCTAAAGCTCCATGTCTCTGGG 1720
QY 1384 CTTAAATTCGTATAAATCTGGATTTTTTTTTTTTTTTTTTGTCTCATATTTCAATATGTAA 1443
Db 1721 CTTAAATTCGTATAAATCTGGATTTTTTTTTTTTTTTTTTGTCTCATATTTCAATATGTAA 1780
QY 1444 ACCAGAACATTTCTATGTACTACAAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGAAT 1503
Db 1781 ACCAGAACATTTCTATGTACTACAAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGAAT 1840
QY 1504 TAAACTTGTGTAGTGTGATAGGACAGACTGGA 1536

APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Guiney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C331
CURRENT APPLICATION NUMBER: PCT/US01/43523
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 285
LENGTH: 2845
TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: unsure
LOCATION: 2715
OTHER INFORMATION: unknown base
PCT-US01-43523-285

Query Match 99.8%; Score 1532.6; DB 1; Length 2849;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAAATATCCAGTTTCCAGCAACAGGACAGGAGTACAGATCTCAGCATGAGA 63
Db 367 GAAATATCCAGTTTCCAGCAACAGGACAGGAGTACAGATCTCAGCATGAGA 426
QY 64 GAAATATCCAGTTTCCAGCAACAGGAGTACAGATCTCAGCATGAGA 123
Db 427 GAAATATCCAGTTTCCAGCAACAGGAGTACAGATCTCAGCATGAGA 486
QY 124 CAAGAAATCCGTTCTGGTATGGAGATTAGTAGCAGTAGAGAAATATGATGATCAAC 183
Db 487 CAAGAAATCCGTTCTGGTATGGAGATTAGTAGCAGTAGAGAAATATGATGATCAAC 546
QY 184 TTACGTTTGGATGAAGATTGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
Db 547 TTACGTTTGGATGAAGATTGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 606
QY 244 TTGTAGAAAGTTGAGGAACCCAGTATGGAACACTATATTAGGGCGCTGGTCTGGTA 303

607 TTGTAGAAAGTTGAGGAACCCAGTATGGAACACTATATTAGGGCGCTGGTCTGGTA 666
QY 304 CTGTACCCAGGAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTGTATCTGATG 363
Db 667 CTGTACCCAGGAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTGTATCTGATG 726
QY 364 AATATTTTCTGTGAACCCAGGTTCTGCATCCACTACAACTTGTGATGCGCAATTC 423
Db 727 AATATTTTCTGTGAACCCAGGTTCTGCATCCACTACAACTTGTGATGCGCAATTC 786
QY 424 CAGAAGCTGTGAGTCCCTTCAAGTCTACCCCTTCAAGTCTTGGCACTGGACCTCTTAATA 483
Db 787 CAGAAGCTGTGAGTCCCTTCAAGTCTACCCCTTCAAGTCTTGGCACTGGACCTCTTAATA 846
QY 484 ATGCTATACTGCTTTAGTACCTTGAAGACCTTATTCATATCTTGAACAGAGAT 543
Db 847 ATGCTATACTGCTTTAGTACCTTGAAGACCTTATTCATATCTTGAACAGAGAT 906
QY 544 GGCAGTTTGGACTTAGAAGATCTATATAGGCCAACTTGGCACTTCTTGGCAAGCTTTTG 603
Db 907 GGCAGTTTGGACTTAGAAGATCTATATAGGCCAACTTGGCACTTCTTGGCAAGCTTTTG 966
QY 604 TTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTTAAACAGAGAGTAAATAT 663
Db 967 TTTTGGAGAAATCCAGAGTGGTGGATCTGAACCTTCTTAAACAGAGAGTAAATAT 1026
QY 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACCGATA 723
Db 1027 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGGAAGAACTAAAGAGAACCGATA 1086
QY 724 CCATTTTCTGGCCAGGTTGTCTCTGTTAAACGCTGTGTGGGAACTGTGCCCTTTGTC 783
Db 1087 CCATTTTCTGGCCAGGTTGTCTCTGTTAAACGCTGTGTGGGAACTGTGCCCTTTGTC 1146
QY 784 TCCAAATTCGAATGAATGTCAATGTGTCCAAAGCAAGTTACTTAAATAATACACAGG 843
Db 1147 TCCAAATTCGAATGAATGTCAATGTGTCCAAAGCAAGTTACTTAAATAATACACAGG 1206
QY 844 TCCTTCAGTTTGAACCAACAAACCGGTGTGAGGGGATGCAACAATCACTCACCAAGTGG 903
Db 1207 TCCTTCAGTTTGAACCAACAAACCGGTGTGAGGGGATGCAACAATCACTCACCAAGTGG 1266
QY 904 CCTGGAGCACCATGAGGAGTGTGACTGTGTGCGAGAGGAGACACAGGAGGATAGCCGC 963
Db 1267 CCTGGAGCACCATGAGGAGTGTGACTGTGTGCGAGAGGAGACACAGGAGGATAGCCGC 1326
QY 964 ATCACCAACAGCAGCTCTTCCCGCAGAGCTGTGCGAGTGCAGTGTGATTTAGAGAA 1023
Db 1327 ATCACCAACAGCAGCTCTTCCCGCAGAGCTGTGCGAGTGCAGTGTGATTTAGAGAA 1386
QY 1024 CGTATGCGTTATCTCCATCCTTAATCTCAGTGTGTTGTTGTTCAAGGACCTTTCTCTCAG 1083
Db 1387 CGTATGCGTTATCTCCATCCTTAATCTCAGTGTGTTGTTGTTCAAGGACCTTTCTCTCAG 1446
QY 1084 GATTTCAGTGCATCTCGAAGAGGAGACATCAACAGATTAAGGAGTCTGCAACAGCT 1143
Db 1447 GATTTCAGTGCATCTCGAAGAGGAGACATCAACAGATTAAGGAGTCTGCAACAGCT 1506
QY 1144 CTTTGTAGAGAGGAGGCTTAAAGGAGCAGGAGAAAGGCTCTTCAATCGTGGAAAGAAATTA 1203
Db 1507 CTTTGTAGAGAGGAGGCTTAAAGGAGCAGGAGAAAGGCTCTTCAATCGTGGAAAGAAATTA 1566
QY 1204 ATGTTGTATTAATAGATCACAGCTAGTTTCAAGTTCACATGATGATTTCCATAGC 1263
Db 1567 ATGTTGTATTAATAGATCACAGCTAGTTTCAAGTTCACATGATGATTTCCATAGC 1626
QY 1264 TGGTCTCTGATTTTCAAGTCTTTCGATACCGCTTGGGTAATCTCAGTACAGGAAATA 1323
Db 1627 TGGTCTCTGATTTTCAAGTCTTTCGATACCGCTTGGGTAATCTCAGTACAGGAAATA 1686
QY 1324 CTGTGCAAGTGAACACCTGATTCCTGTTGCTTAACTCTTAAAGCTTCAAGCTCTCTGGG 1383


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Db 1387 CGTATCGTTATCTCCATCTTAATCTCAGTTGTTTGGTTCAGGACCTTTTCATCTTCAG 1446
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QY 1144 CTTTTCAGAGGAGGCTTAAAGGACAGAGAAAGGCTTCAATCGTGGAAAGAAATTTAA 1203
Db 1507 CTTTTCAGAGGAGGCTTAAAGGACAGAGAAAGGCTTCAATCGTGGAAAGAAATTTAA 1566
QY 1204 ATGTTGTTAATATAGATCACACAGCTAGTTTTCAGAGTTACCATGTACGTATTCCTAGC 1263
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Db 1627 TGGTTCTGTTATTCAGTTCTTTTCGATACGGCTTACGGTAAATGTACAGTACAGAGAAAAA 1686
QY 1324 CTGTGCAAGTGACACCTGATTCGGTTGCTTAACTCTAAAGCTCCATGTCCTGGG 1383
Db 1687 CTGTGCAAGTGACACCTGATTCGGTTGCTTAACTCTAAAGCTCCATGTCCTGGG 1746
QY 1384 CCTAAATCGTATAAAATCTGGAATTTTTTTTTTTTTTTTTTTTGGTCTCATATGTA 1443
Db 1747 CCTAAATCGTATAAAATCTGGAATTTTTTTTTTTTTTTTTTTTGGTCTCATATGTA 1806
QY 1444 ACCAGACATCTATGTACTACAACTGGTTTAAAGGAAAGTATGCTATGTA 1503
Db 1807 ACCAGACATCTATGTACTACAACTGGTTTAAAGGAAAGTATGCTATGTA 1866
QY 1504 TAAACTTGTCTATGCTGATAGGACAGACTGGA 1536
Db 1867 TAACTTGTCTATGCTGATAGGACAGACTGGA 1899
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RESULT 13

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PCT-US01-43523-285
; Sequence 285, Application PC/TUS0143523
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Guney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCES: P3330R1C331
; CURRENT APPLICATION NUMBER: PCT/US01/43523
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 285
; LENGTH: 2849
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2715
; OTHER INFORMATION: unknown base
PCT-US01-43523-285
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Query Match 99.8%; Score 1532.6; DB 2; Length 2849;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 GTAAATTCAGTTCCTCCAGCAACAGAGGAAACAGAGGAGTACAAAGATCCTCAGCATGAGA 63
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QY 124 CAAGAAATACGCTCTTGGTATGAGATTTAGTAGCAGTAGAGGAAATCTATGGATACAAAC 183
Db 487 CAAGAAATACGCTCTTGGTATGAGATTTAGTAGCAGTAGAGGAAATCTATGGATACAAAC 546
QY 184 TTACGTTTTCATCAAGATTTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
Db 547 TTACGTTTTCATCAAGATTTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 606
QY 244 TTGTAGAAAGTTGAGGAAACCCAGATGAGAACTATATATTAGGGCGCTGGTGGTCTGGTA 303
Db 607 TTGTAGAAAGTTGAGGAAACCCAGATGAGAACTATATATTAGGGCGCTGGTGGTCTGGTA 666
QY 304 CTGTACCAAGGAAACAGAGTTTCTAAAGGAAATCAAAATTAGGATAGATTTCTATCTGATG 363
Db 667 CTGTACCAAGGAAACAGAGTTTCTAAAGGAAATCAAAATTAGGATAGATTTCTATCTGATG 726
QY 364 AATATTTTCTTCGAAACAGGTTTCTGCATCCACTACAACTGTCATGCCAATTC 423
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QY 424 CAGAAGCTGTGAGTCTTCAGTGTCTACCCCTTCAGCTTTCCACTGACCTGCTTAATA 483
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QY 484 ATGCTATAACTGCCCTTTAGTACCTTTGGAAAGCTTTATTCGATATCTTTGAAACAGAGAGAT 543
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Db 1027 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAAGAACTAAAGAGAACCGATA 1086
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Qy	724	CCATTTTC	TGCGC	AGGTGTG	CTCCTCG	TTAAAC	CGTGTG	GGAACT	GTGCC	TTGTGC	783
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Qy	784	TCCCAAT	TGCAAT	TGATGT	CAATGT	GTGCC	CAAGCA	AAGTTT	TACTAA	AAAAAT	843
Db	1147	TCCCAAT	TGCAAT	TGATGT	CAATGT	GTGCC	CAAGCA	AAGTTT	TACTAA	AAAAAT	1206
Qy	844	TCCTTC	AGTTG	AGAC	CCAAAS	ACCGGT	GTFC	AGGGAT	TGC	CAAAAT	903
Db	1207	TCCTTC	AGTTG	AGAC	CCAAAG	ACCGGT	GTFC	AGGGAT	TGC	CAAAAT	1266
Qy	904	CCCTG	GGAC	CCATG	AGGAG	TGTCA	CTGTG	TGTC	GAGG	GAGCAC	963
Db	1267	CCCTG	GGAC	CCATG	AGGAG	TGTCA	CTGTG	TGTC	GAGG	GAGCAC	1326
Qy	964	ATCACC	ACC	AGCAG	CTCTT	GCC	CAGAG	CTGTG	CAGT	TGGCTG	1023
Db	1327	ATCACC	ACC	AGCAG	CTCTT	GCC	CAGAG	CTGTG	CAGT	TGGCTG	1386
Qy	1024	CGTAT	GCG	TATCT	CCAT	TCC	TAACT	CTC	AGT	TGTTG	1083
Db	1387	CGTAT	GCG	TATCT	CCAT	TCC	TAACT	CTC	AGT	TGTTG	1446
Qy	1084	GATTTA	CAG	TGCATT	CTTGA	AGAG	GAGAC	ATCA	AA	CAGAA	1143
Db	1447	GATTTA	CAG	TGCATT	CTTGA	AGAG	GAGAC	ATCA	AA	CAGAA	1506
Qy	1144	CTTTTG	AGAG	GAGC	CTTAA	AGG	CAGG	AAAA	AGGCT	TTCA	1203
Db	1507	CTTTTG	AGAG	GAGC	CTTAA	AGG	CAGG	AAAA	AGGCT	TTCA	1566
Qy	1204	ATGTTG	TATTA	ATAG	ATCA	CCAG	CTAG	TTT	CAGAG	TAC	1263
Db	1567	ATGTTG	TATTA	ATAG	ATCA	CCAG	CTAG	TTT	CAGAG	TAC	1626
Qy	1264	TGGGTT	CTGT	TATTT	CAGT	CTCTT	CGAT	CAGC	TTT	AGG	1323
Db	1627	TGGGTT	CTGT	TATTT	CAGT	CTCTT	CGAT	CAGC	TTT	AGG	1686
Qy	1324	CTGTG	CAAG	TGAG	CAC	CTG	ATTC	CGT	TG	CTTAA	1383
Db	1687	CTGTG	CAAG	TGAG	CAC	CTG	ATTC	CGT	TG	CTTAA	1746
Qy	1384	CCCTAA	ATCG	TATAA	ATCT	GGA	TTTTTTTT	TTTTTTTT	TTTTTT	TGCT	1443
Db	1747	CCCTAA	ATCG	TATAA	ATCT	GGA	TTTTTTTT	TTTTTTTT	TTTTTT	TGCT	1806
Qy	1444	ACCAGA	A	CATTCT	ATGT	PACT	CA	AAAC	CTGG	TTTTT	1503
Db	1807	ACCAGA	A	CATTCT	ATGT	PACT	CA	AAAC	CTGG	TTTTT	1866
Qy	1504	TAAACT	TG	TGTC	ATG	CTG	ATG	AGAC	AG	CTGGA	1536
Db	1867	TAAACT	TG	TGTC	ATG	CTG	ATG	AGAC	AG	CTGGA	1899

RESULT 14

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US-09-267-213-1
; Sequence 1, Application US/09267213
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Ferrara, Audrey
; APPLICANT: Goddard, Austrey
; APPLICANT: Gurney, Austin
; APPLICANT: Hebert, Caroline
; APPLICANT: Henzel, William
; APPLICANT: Kabakoff, Rhona
; APPLICANT: Klein, Robert D.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Lafleur, Monique
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Method of Preventing the Death of Retinal Neurons and

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1 PRIOR APPLICATION NUMBER: US 60/082,700
2 PRIOR FILING DATE: 1998-04-22
3 PRIOR APPLICATION NUMBER: US 60/082,804
4 PRIOR FILING DATE: 1998-04-22
5 PRIOR APPLICATION NUMBER: US 60/082,704
6 PRIOR FILING DATE: 1998-04-22
7 PRIOR APPLICATION NUMBER: US 60/082,767
8 PRIOR FILING DATE: 1998-04-23
9 PRIOR APPLICATION NUMBER: US 60/082,796
10 PRIOR FILING DATE: 1998-04-23
11 PRIOR APPLICATION NUMBER: US 60/083,336
12 PRIOR FILING DATE: 1998-04-27
13 PRIOR APPLICATION NUMBER: US 60/083,322
14 PRIOR FILING DATE: 1998-04-28
15 PRIOR APPLICATION NUMBER: US 60/083,392
16 PRIOR FILING DATE: 1998-04-29
17 PRIOR APPLICATION NUMBER: US 60/083,499
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23 PRIOR APPLICATION NUMBER: US 60/083,495
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33 PRIOR APPLICATION NUMBER: US 60/083,742
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48 PRIOR FILING DATE: 1998-05-07
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67 PRIOR APPLICATION NUMBER: US 60/085,579
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1 PRIOR FILING DATE: 1998-05-15
2 PRIOR APPLICATION NUMBER: US 60/085,700
3 PRIOR FILING DATE: 1998-05-15
4 PRIOR APPLICATION NUMBER: US 60/086,023
5 PRIOR FILING DATE: 1998-05-18
6 PRIOR APPLICATION NUMBER: US 60/086,486
7 PRIOR FILING DATE: 1998-05-22
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9 PRIOR FILING DATE: 1998-05-22
10 PRIOR APPLICATION NUMBER: US 60/086,392
11 PRIOR FILING DATE: 1998-05-22
12 PRIOR APPLICATION NUMBER: US 60/086,430
13 PRIOR FILING DATE: 1998-05-22
14 PRIOR APPLICATION NUMBER: US 60/087,208
15 PRIOR FILING DATE: 1998-05-28
16 PRIOR APPLICATION NUMBER: US 60/087,098
17 PRIOR FILING DATE: 1998-05-28
18 PRIOR APPLICATION NUMBER: US 60/087,106
19 PRIOR FILING DATE: 1998-05-28
20 PRIOR APPLICATION NUMBER: US 60/094,651
21 PRIOR FILING DATE: 1998-07-30
22 PRIOR APPLICATION NUMBER: US 60/100,038
23 PRIOR FILING DATE: 1998-09-11
24 NUMBER OF SEQ ID NOS: 538
25 SEQ ID NO 487
26 LENGTH: 2849
27 TYPE: DNA
28 ORGANISM: Homo sapiens
29 FEATURE:
30 NAME/KEY: unsure
31 LOCATION: 2715
32 OTHER INFORMATION: unknown base
33 US-09-380-138-487

Query Match 99.8%; Score 1532.6; DB 20; Length 2849;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTAAATTCAGTTTTCCAGCAACAGAGGAAACAGAGGAGTACAGATCCTCAGCATGAGA 63
DB 367 GTAATTCAGTTTTCCAGCAACAGAGGAAACAGAGGAGTACAGATCCTCAGCATGAGA 426
QY 64 GAATTTACTGTGTCTACTAATGGAAGTATTCAGCCCAAGGTTTCTCATCTTATC 123
DB 427 GAATTTACTGTGTCTACTAATGGAAGTATTCAGCCCAAGGTTTCTCATCTTATC 486
QY 124 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATGTATGGATACAC 183
DB 487 CAAGAAATACCGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAATGTATGGATACAC 546
QY 184 TTACGTTTGTATGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
DB 547 TTACGTTTGTATGAAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 606
QY 244 TTGTAGAAGTTTCAGGAACCCAGTGTGAACTATATTTAGGGCGCTGGTGTCTGTGTA 303
DB 607 TTGTAGAAGTTTCAGGAACCCAGTGTGAACTATATTTAGGGCGCTGGTGTCTGTGTA 666
QY 304 CTGTACCCAGGAAACAGAGTTTCTTAAGGAAATCAAATTTAGGATAGATTTGTATCTGATG 363
DB 667 CTGTACCCAGGAAACAGAGTTTCTTAAGGAAATCAAATTTAGGATAGATTTGTATCTGATG 726
QY 364 AATATTTCTTCTGAAACCCAGGTTTCTGATCCACTACACATTTGTCATGCCAATTCAC 423
DB 727 AATATTTCTTCTGAAACCCAGGTTTCTGATCCACTACACATTTGTCATGCCAATTCAC 786
QY 424 CAGAGCTGTGAGTCTTTCAGTGTACCCCTTCAGCTTCCACTGACCTGCTTATA 483
DB 787 CAGAGCTGTGAGTCTTTCAGTGTACCCCTTCAGCTTCCACTGACCTGCTTATA 846
QY 484 ATGCTATAACTGCCCTTTAGTACCTTTGGAGACCTTTATTCGATATCTTTGAACACAGAGAT 543
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1531	99.7	3007	1	PCT-US03-26491-58
2	1531	99.7	3007	6	US-10-648-593-58
3	1531	99.7	3007	7	US-60-487-610-231
4	1531	99.7	3007	7	US-60-485-450-137
5	1531	99.7	3007	7	US-60-507-511-2084
6	1529.4	99.6	2779	5	US-09-830-320A-8
7	1511	98.4	1760	5	US-09-457-066-1
8	1511	98.4	1760	5	US-09-876-813-32
9	1511	98.4	1760	5	US-10-664-432-1
10	955.6	62.2	1095	5	US-09-457-066-50
11	721	46.9	3571	5	US-09-457-066-42
12	721	46.9	3571	5	US-09-876-813-34
13	721	46.9	3571	5	US-10-664-432-3
14	694.4	45.2	221510	7	US-60-487-610-19346
15	694.4	45.2	221510	7	US-60-485-450-11913
16	684.4	44.6	1035	5	US-09-457-066-6
17	621	40.4	918	1	PCT-US00-28803-6
18	200.6	13.1	201	7	US-60-487-610-5054
19	200.6	13.1	201	7	US-60-487-610-5055
20	200.6	13.1	201	7	US-60-487-610-32070
21	200.6	13.1	201	7	US-60-487-610-32126
22	200.6	13.1	201	7	US-60-485-450-3280
23	200.6	13.1	201	7	US-60-485-450-3281
24	200.6	13.1	201	7	US-60-485-450-19014
25	200.6	13.1	201	7	US-60-485-450-19070
26	200.2	13.0	201	7	US-60-487-610-5053

27	200.2	13.0	201	7	US-60-487-610-32074	Sequence 32074, A
28	200.2	13.0	201	7	US-60-485-450-3279	Sequence 3279, AP
29	200.2	13.0	201	7	US-60-485-450-19018	Sequence 19018, A
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32	120.6	7.9	201	7	US-60-487-610-5052	Sequence 5052, AP
33	120.6	7.9	201	7	US-60-487-610-32073	Sequence 32073, A
34	120.6	7.9	201	7	US-60-485-450-3278	Sequence 3278, AP
35	120.6	7.9	201	7	US-60-485-450-19017	Sequence 19017, A
36	117.4	7.6	1113	6	US-10-321-962-7	Sequence 7, Appli
37	117.4	7.6	1472	5	US-09-876-813-52	Sequence 52, Appli
38	117.4	7.6	1472	6	US-10-606-055-3	Sequence 3, Appli
39	105.2	6.8	1829	6	US-10-321-962-3	Sequence 36, Appli
40	103.6	6.7	1882	5	US-09-457-066-36	Sequence 36, Appli
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42	103.6	6.7	1882	6	US-10-606-055-1	Sequence 1, Appli
43	101.4	6.6	1587	6	US-10-321-962-5	Sequence 5, Appli
44	85.6	5.6	898	6	US-10-321-962-9	Sequence 9, Appli
45	84	5.5	462	6	US-10-321-962-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1

PCT-US03-26491-58
; Sequence 58, Application PC/TUS0326491
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS TH
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; FILE REFERENCE: D0273 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/26491
; CURRENT FILING DATE: 2003-08-26
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 58
; LENGTH: 3007
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-26491-58

Query Match	99.7%	Score 1531;	DB 1;	Length 3007;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 1531;	Conservative	1;	Mismatches	1;
			Indels	0;
			Gaps	0;
Qy	4	GTAATTCAGTTTTCAGCAACAGGACAGAGACGAGTACAGATCCTCAGCATGAGA	63	
Db	574	GTAATTCAGTTTTCAGCAACAGGACAGAGACGAGTACAGATCCTCAGCATGAGA	633	
Qy	64	GAATTTACTGTGTCTACTAATGGAATTTACAGCCCAAGGTTTCTCTACTACTTATC	123	
Db	534	GAATTTACTGTGTCTACTAATGGAATTTACAGCCCAAGGTTTCTCTACTACTTATC	693	
Qy	124	CAAGAAATACGGTCTTGATGAGATTTAGTACAGTAGAGGAAATGTATGATACAC	183	
Db	694	CAAGAAATACGGTCTTGATGAGATTTAGTACAGTAGAGGAAATGTATGATACAC	753	
Qy	184	TTACGTTTGAATGAAGATTTGGCTTGAGACCCAGGATGACATATGCAAGTATGATT	243	
Db	754	TTACGTTTGAATGAAGATTTGGCTTGAGACCCAGGATGACATATGCAAGTATGATT	813	
Qy	244	TTGTAGAAGTTGAGGAACCCAGTGTAGTGAATCTATATTAGGGCGCTGGTGTGGTGA	303	
Db	814	TTGTAGAAGTTGAGGAACCCAGTGTAGTGAATCTATATTAGGGCGCTGGTGTGGTGA	873	
Qy	304	CTGTACAGGAAACAGATTTCTAAAGGAAATCAATATTAGGATAAGATTTGATCTGATG	363	
Db	874	CTGTACAGGAAACAGATTTCTAAAGGAAATCAATATTAGGATAAGATTTGATCTGATG	933	

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Qy	664	ACAGCTGCACACTCGTACTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA	723
Db	1234	ACAGCTGCACACTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA	1293
Qy	724	CCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACCGCTGTGGTGGGAACTGTGCTGTGTGC	783
Db	1294	CCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACCGCTGTGGTGGGAACTGTGCTGTGTGC	1353
Qy	784	TCCACAAATTCGAATGATGTCAATGTGTCCTCCAGCAAGATTTCTAAATAATCCACGAGG	843
Db	1354	TCCACAAATTCGAATGATGTCAATGTGTCCTCCAGCAAGATTTCTAAATAATCCACGAGG	1413
Qy	844	TCCTTCAGTTTGAGACCAASACCGGTGTCTAGGGGATTGCACAAATCACTCACCGACGTGG	903
Db	1414	TCCTTCAGTTTGAGACCAAGACCGGTGTCTAGGGGATTGCACAAATCACTCACCGACGTGG	1473
Qy	904	CCCTGGAGCACCATGAGGATGTGACTGTGTGTCAGAGGAGACACAGGAGGATACCCGC	963
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Db	1894	CTGTGCAAGTGAGCACCTCGATTCCGTTTGCCTTGCTTAACTTAAAGCTCCATGTCTCTGGG	1953
Qy	1384	CCTAAATACGTATATAAATCTGGATTTTTTTTTTTTTTTTTTTTTTGTCTCATATTACATATGTAA	1443
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Qy	1444	ACCAGAACTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGTAAT	1503
Db	2014	ACCAGAACTTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGTAAT	2073
Qy	1504	TAAACTGTGTGTCATGCTGATAGGACAGACTGGA	1536
Db	2074	TAAACTGTGTGTCATGCTGATAGGACAGACTGGA	2106

Db	1294	CCATTTTCTGCGCAGGTTGTCTCTGTGTTAAACGCTGTGCTGGGAACTGTGCTCTGTTGTC	1353
Qy	784	TCCCAANTTGCATGATGTCATATGTCGTCCTCCAGCAAAGTTACTTAAAAATATCCACAGG	843
Db	1354	TCCCAAAATTGCATGAAATGTCATATGTCCTCCAGCAAAGTTACTTAAAAATATCCACAGG	1413
Qy	844	TCCTTCACAGTTGAGACCAAAASACCGGTCTCAGGGGATTCGCAAAATCACTCACCGACGTGG	903

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RESULT 3
US-60-487-610-231
; Sequence 231, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,

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1414 1414 TCTTCAGTTGAGCAAAAGCCGGTGTGAGGGATTGCAAAATCACTCACCGAGCTGG 1473
QY
904 CCTTGAGCACCATGAGGAGTGTGCTGTGTCAGAGGGAGCACAGAGATAGCCGC 963
Db
1474 CCTTGAGCACCATGAGGAGTGTGCTGTGTCAGAGGGAGCACAGAGATAGCCGC 1533
QY
964 ATCACCACAGCAGCTCTTGGCCAGAGCTGTGCTGAGTGGCTGATTCTATTAGAGAA 1023
Db
1534 ATCACCACAGCAGCTCTTGGCCAGAGCTGTGCTGAGTGGCTGATTCTATTAGAGAA 1593
QY
1024 CGTATCGTTATCTCATCTTAATCTGATGTTGCTTCAAGACCTTTCATCTTCAAG 1083
Db
1594 CRTATCGTTATCTCATCTTAATCTGATGTTGCTTCAAGACCTTTCATCTTCAAG 1653
QY
1084 GATTTACAGTGCATCTGAAAGAGGAGACATCAACAGAAATTAGAGATTGTCAACAGCT 1143
Db
1654 GATTTACAGTGCATCTGAAAGAGGAGACATCAACAGAAATTAGAGATTGTCAACAGCT 1713
QY
1144 CTTTGGAGAGGAGCTTAAAGGAGCAGGAGAAAGGCTTCAATCTGTTGAAAGAAATTA 1203
Db
1714 CTTTGGAGAGGAGCTTAAAGGAGCAGGAGAAAGGCTTCAATCTGTTGAAAGAAATTA 1773
QY
1204 ATGTTGATTAAATAGATCAACAGCTAGTTTCAAGATTACCATGACGTATTCACAGC 1263
Db
1774 ATGTTGATTAAATAGATCAACAGCTAGTTTCAAGATTACCATGACGTATTCACAGC 1833
QY
1264 TGGGTTCTGATTTCAAGTCTTTCGATACGGCTTAGGTAATGTGAGTACAGAGAAATA 1323
Db
1834 TGGGTTCTGATTTCAAGTCTTTCGATACGGCTTAGGTAATGTGAGTACAGAGAAATA 1893
QY
1324 CTGTGCAAGTGAGCAGCTGATTCGTTGCTTAACTTAAAGTCTCAATGCTGCTGG 1383
Db
1894 CTGTGCAAGTGAGCAGCTGATTCGTTGCTTAACTTAAAGTCTCAATGCTGCTGG 1953
QY
1384 CTTAAATCGTATTAATCTGATTTTCTGATTTTCTGATTTTCTGATTTTCTGATTTT 1443
Db
1954 CTTAAATCGTATTAATCTGATTTTCTGATTTTCTGATTTTCTGATTTTCTGATTTT 2013
QY
1444 ACCAGAACATCTATGATACAGCTGATTAAGCTGTTTAAAGGAGACTATGCTGATGAT 1503
Db
2014 ACCAGAACATCTATGATACAGCTGATTAAGCTGTTTAAAGGAGACTATGCTGATGAT 2073
QY
1504 TAAACTTGTCTCATGCTGATGAGCAGACTGGA 1536
Db
2074 TAAACTTGTCTCATGCTGATGAGCAGACTGGA 2106

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RESULT 4

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US-60-485-450-137
; Sequence 137, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-Yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: GI001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 137
; LENGTH: 3007
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-485-450-137

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Query Match 99.7%; Score 1531; DB 7; Length 3007;
Best local Similarity 99.7%; Pred. No. 0;
Matches 1528; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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QY 4 GTAAATTCAGTTTTCAGCAACAGGAACAGAGTACAGATCCTCAGCATGAGA 63
Db 574 GTAAATTCAGTTTTCAGCAACAGGAACAGAGTACAGATCCTCAGCATGAGA 633
QY 64 GAATTTATCTGTGTCTTACTTAATGGAAGTATTCACAGCCCAAGGTTTCTCATACTATC 123
Db 634 GAATTTATCTGTGTCTTACTTAATGGAAGTATTCACAGCCCAAGGTTTCTCATACTATC 693
QY 124 CAAGAAATACGGTCTTGGTATGAGATTTAGTAGAGTAGAGGAAATGTATGATCAAC 183
Db 694 CAAGAAATACGGTCTTGGTATGAGATTTAGTAGAGTAGAGGAAATGTATGATCAAC 753
QY 184 TTACGTTTGTATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
Db 754 TTACGTTTGTATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 813
QY 244 TTGTAGAAGTTGAGGAACCCAGAGTGTGAACTATATTTAGGGCGCTGGTGTGGTAT 303
Db 814 TTGTAGAAGTTGAGGAACCCAGAGTGTGAACTATATTTAGGGCGCTGGTGTGGTAT 873
QY 304 CTGTACAGAGAAACAGATTTCTAAGGAAATCAAAATAGGATAAGATTTGTATCTGATG 363
Db 874 CTGTACAGAGAAACAGATTTCTAAGGAAATCAAAATAGGATAAGATTTGTATCTGATG 933
QY 364 AATATTTTCTTCTGAACACAGGGTTCTGCATCCACTACAACTTGTCTATGCCCAATTC 423
Db 934 AATATTTTCTTCTGAACACAGGGTTCTGCATCCACTACAACTTGTCTATGCCCAATTC 993
QY 424 CAGAAGCTGTGAGTCTTCTGATGCTACCCCTTTCAGCTTTGCCACTGGAACCTGCTTAATA 483
Db 994 CAGAAGCTGTGAGTCTTCTGATGCTACCCCTTTCAGCTTTGCCACTGGAACCTGCTTAATA 1053
QY 484 ATGCTATTAATCTGCTTGTAGTACCTTGAAGACCTTATTCGATATCTTGAACACAGAGAT 543
Db 1054 ATGCTATTAATCTGCTTGTAGTACCTTGAAGACCTTATTCGATATCTTGAACACAGAGAT 1113
QY 544 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGCTTTTG 603
Db 1114 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGCTTTTG 1173
QY 604 TTTTGGAGAAATACAGAGTGTGATCTGAACCTTCTAAGAGAGAGTATGATAT 663
Db 1174 TTTTGGAGAAATACAGAGTGTGATCTGAACCTTCTAAGAGAGAGTATGATAT 1233
QY 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA 723
Db 1234 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA 1293
QY 724 CCATTTCTGCGCAGGTTGCTCCTGGTTAAACGCTGTGGTGGAACTGTGCTGTTGTC 783
Db 1294 CCATTTCTGCGCAGGTTGCTCCTGGTTAAACGCTGTGGTGGAACTGTGCTGTTGTC 1353
QY 784 TCCCAATTTGCAATGAATGTCAATGTCTCCCAAGCAAGTTTACTTAAATAATACCAAGG 843
Db 1354 TCCCAATTTGCAATGAATGTCAATGTCTCCCAAGCAAGTTTACTTAAATAATACCAAGG 1413
QY 844 TCCTTCAGTTGAGACCAAAACCCGGTGTGAGGGGATTTGCAAAATCACTACCCGACGTGG 903
Db 1414 TCCTTCAGTTGAGACCAAAACCCGGTGTGAGGGGATTTGCAAAATCACTACCCGACGTGG 1473
QY 904 CCCTGGAGCACCATGAGGAGTGTGACCTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGC 963
Db 1474 CCCTGGAGCACCATGAGGAGTGTGACCTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGC 1533
QY 964 ATCACCACAGCAGCTCTTGGCCAGAGCTGTGAGTGCAGTGGCTGATTTCTATTAGAGAA 1023
Db 1534 ATCACCACAGCAGCTCTTGGCCAGAGCTGTGAGTGCAGTGGCTGATTTCTATTAGAGAA 1593
QY 1024 CGTATGCTTATCTCATCTTAATCTGATGTTGCTTCAAGACCTTTCATCTTCAAG 1083
Db 1594 CRTATGCTTATCTCATCTTAATCTGATGTTGCTTCAAGACCTTTCATCTTCAAG 1653
QY 1084 GATTTACAGTGCATCTGAAAGAGGAGACATCAACAGAAATTAGAGATTGTGCAACAGCT 1143

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Db 1654 GAATTTACAGTGCATTCGAAAGAGGAGACATCAACAGAAATTAGAGATTGGCAACAGCT 1713
Qy 1144 CTTTTCAGAGGAGGCTAAAGACAGGAGAAAGGTCTTCAATCGTGGAAGAAATPAA 1203
Db 1714 CTTTTCAGAGGAGGCTAAAGACAGGAGAAAGGTCTTCAATCGTGGAAGAAATPAA 1773
Qy 1204 ATGTTGTATTAATAGATCACAGCTAGTTTCAGAGTTACCATGTATTCACATGAC 1263
Db 1774 ATGTTGTATTAATAGATCACAGCTAGTTTCAGAGTTACCATGTATTCACATGAC 1833
Qy 1264 TGGGTTCTGATTTTCAGTTCTTTCGATACGGCTTAGGGTAAATGTCACTACAGGAAAAAA 1323
Db 1834 TGGGTTCTGATTTTCAGTTCTTTCGATACGGCTTAGGGTAAATGTCACTACAGGAAAAAA 1893
Qy 1324 CTGTGCAAGTAGACCTGATTCGGTTGCTTGTCTTAATCTAAAGCTCCATGCTCTGGG 1383
Db 1894 CTGTGCAAGTAGACCTGATTCGGTTGCTTGTCTTAATCTAAAGCTCCATGCTCTGGG 1953
Qy 1384 CCTAAAATCGTATAAAATCTGGATTTTCTTTTCTGCTCATATTCACATATGAA 1443
Db 1954 CCTAAAATCGTATAAAATCTGGATTTTCTTTTCTGCTCATATTCACATATGAA 2013
Qy 1444 ACCAGAACATTCATGTACTACAAACCTGTTTAAAGAACTATGTTGCTATGAAT 1503
Db 2014 ACCAGAACATTCATGTACTACAAACCTGTTTAAAGAACTATGTTGCTATGAAT 2073
Qy 1504 TAAACTGTGCTCATGCTAGTAGACAGACTGGA 1536
Db 2074 TAAACTGTGCTCATGCTAGTAGACAGACTGGA 2106

RESULT 5
US-60-507-511-2084
; Sequence 2084, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2084
; LENGTH: 3007
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-2084

Query Match 99.7%; Score 1531; DB 7; Length 3007;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1531; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GTAAATTCAGTTTCCAGCAACAGGAAACAGAGTACAGATCTCCAGCATGAGA 63
Db 574 GTAAATTCAGTTTCCAGCAACAGGAAACAGAGTACAGATCTCCAGCATGAGA 633
Qy 64 GAATTTACTGTGCTACTAATGGAAGTATTACAGGCCCAAGGTTTCTCATCTATC 123
Db 634 GAATTTACTGTGCTACTAATGGAAGTATTACAGGCCCAAGGTTTCTCATCTATC 693
Qy 124 CAAGAAATACGGTCTTGGTATGAGATTAGTAGCAGTAGAGGAAATGTATGATACAC 183
Db 694 CAAGAAATACGGTCTTGGTATGAGATTAGTAGCAGTAGAGGAAATGTATGATACAC 753
Qy 184 TTACGTTTGTATGAAGATTGGGCTTGAAGACCCAGAGTACATATGCAAGTATGATT 243
Db 754 TTACGTTTGTATGAAGATTGGGCTTGAAGACCCAGAGTACATATGCAAGTATGATT 813
Qy 244 TTGTAGAGTTGAGGAACCCAGTATGGAACCTATATTAGGCGCTGGTGGTCTCGGTA 303

Db 814 TTGTAGAGTTGAGBACCAGTCAGTAACTATATTAGGGCGTGGTGGTCTCGTA 873
Qy 304 CTGTACAGGAAACAGATTTCTAAAGGAAATCAAAATTAGGTAAGATTTGTATCTGATG 363
Db 874 CTGTACAGGAAACAGATTTCTAAAGGAAATCAAAATTAGGTAAGATTTGTATCTGATG 933
Qy 364 AATATTTTCTTCTGAACAGGGTCTGTCACTCACTACAACTATGTCAATGCCCAATTC 423
Db 934 AATATTTTCTTCTGAACAGGGTCTGTCACTCACTACAACTATGTCAATGCCCAATTC 993
Qy 424 CAGAAGCTGTGAGTCTTCACTAGTCTACCCCTTCACTTGGCCATGGAACCTGCTTAATA 483
Db 994 CAGAAGCTGTGAGTCTTCACTAGTCTACCCCTTCACTTGGCCATGGAACCTGCTTAATA 1053
Qy 484 ATGCTATACTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACAGAGAGAT 543
Db 1054 ATGCTATACTGCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACAGAGAGAT 1113
Qy 544 GGCAAGTTGGAATCTAGAAATCTATATAGGCAACTTGGCAACTTCTTGGCAAGCTTTTG 603
Db 1114 GGCAAGTTGGAATCTATATAGGCAACTTGGCAACTTCTTGGCAAGCTTTTG 1173
Qy 604 TTTTGGAGAAATACAGAGTGTGATCTGAACCTTCTAAACAGAGAGGTAAGATTAT 663
Db 1174 TTTTGGAGAAATACAGAGTGTGATCTGAACCTTCTAAACAGAGAGGTAAGATTAT 1233
Qy 664 ACAGCTGCACACCTCTGTAATCTTCTAGTGTCCATAGGGGAAGAACTAAAGAAACCGATA 723
Db 1234 ACAGCTGCACACCTCTGTAATCTTCTAGTGTCCATAGGGGAAGAACTAAAGAAACCGATA 1293
Qy 724 CCAATTTCTGCGCCAGGTTGCTCTCTGTTTAAACGCTGTGTGGAACTGTGCTCTGTTGTC 783
Db 1294 CCAATTTCTGCGCCAGGTTGCTCTCTGTTTAAACGCTGTGTGGAACTGTGCTCTGTTGTC 1353
Qy 784 TCCCAATTTGCAATGAATGTCAATGTCTCCACAGAAAGTTCTAAAGAAATACACACAGG 843
Db 1354 TCCCAATTTGCAATGAATGTCAATGTCTCCACAGAAAGTTCTAAAGAAATACACACAGG 1413
Qy 844 TCCTTCAGTTGAGAACCAACACCGGTGTGAGGGGATTCACAAATCACTCACGACGTGG 903
Db 1414 TCCTTCAGTTGAGAACCAACACCGGTGTGAGGGGATTCACAAATCACTCACGACGTGG 1473
Qy 904 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGC 963
Db 1474 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGC 1533
Qy 964 ATCACACACAGCAGCTCTTGGCCACAGAGCTGTGACGTGACGTGCTGATTCTATTAGAGAA 1023
Db 1534 ATCACACACAGCAGCTCTTGGCCACAGAGCTGTGACGTGACGTGCTGATTCTATTAGAGAA 1593
Qy 1024 CGTAGCGTTATCTCCATCTTAAATCTCAGTTGTTGCTTCAAGGACCTTTTCATCTTCAG 1083
Db 1594 CGTAGCGTTATCTCCATCTTAAATCTCAGTTGTTGCTTCAAGGACCTTTTCATCTTCAG 1653
Qy 1084 GATTTACAGTGCATTTCTGAAGAGGAGACATCAACAGAAATTAGGAGTGTGCAACAGCT 1143
Db 1654 GATTTACAGTGCATTTCTGAAGAGGAGACATCAACAGAAATTAGGAGTGTGCAACAGCT 1713
Qy 1144 CTTTTCAGAGGAGGCTTAAAGGACAGGAGAAAGGTCTTCAATCTGCTGGAAGAAATPAA 1203
Db 1714 CTTTTCAGAGGAGGCTTAAAGGACAGGAGAAAGGTCTTCAATCTGCTGGAAGAAATPAA 1773
Qy 1204 ATGTTGTATTAATAGATCACAGCTAGTTTCAGAGTTACCATGTATTCATCTGAC 1263
Db 1774 ATGTTGTATTAATAGATCACAGCTAGTTTCAGAGTTACCATGTATTCATCTGAC 1833
Qy 1264 TGGGTTCTGATTTTCAGTTCTTTCGATACGGCTTAGGGTAAATGTCACTACAGGAAAAAA 1323
Db 1834 TGGGTTCTGATTTTCAGTTCTTTCGATACGGCTTAGGGTAAATGTCACTACAGGAAAAAA 1893
Qy 1324 CTGTGCAAGTTGAGCAACCTGATTCGGTTGCTTGAACCTTAAAGCTCCATGCTCTGGG 1383
Db 1894 CTGTGCAAGTTGAGCAACCTGATTCGGTTGCTTGAACCTTAAAGCTCCATGCTCTGGG 1953


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Db 1720 CCTAAATCGTATATAATCTGATTTTCTTTTCTCTCATATTCACATATGTA 1779
Qy 1444 ACCGAAACATTTCTATGTACTACAAACCTGGTTTTTAAAGAGAACTATGTTGCTATGAAT 1503
Db 1780 ACCGAAACATTTCTATGTACTACAAACCTGGTTTTTAAAGAGAACTATGTTGCTATGAAT 1839
Qy 1504 TAACTTGTCTATGCTGATAGGACAGACTGGA 1536
Db 1840 TAACTTGTCTGCTGCTGATAGGACAGACTGGA 1872

RESULT 7
US-09-457-066-1
; Sequence 1, Application US/09457066
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-09-457-066-1

Query Match 98.4%; Score 1511; DB 5; Length 1760;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1522; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 4 GTAAATTCAGTTTCCAGCACAGGAGTACAGACCGAGTACAGATCCTCAGCATGAGA 63
Db 236 GTAAATTCAGTTTCCAGCACAGGAGTACAGACCGAGTACAGATCCTCAGCATGAGA 295
Qy 64 GAATATTATCTGTGCTCTAATGGAAGTATTCACAGCCCAAGGTTTCTCCTCATCTTATC 123
Db 296 GAATATTATCTGTGCTCTAATGGAAGTATTCACAGCCCAAGGTTTCTCCTCATCTTATC 355
Qy 124 CAAGAAATACGGTCTTGCTATGAGATTTAGTAGCAGTAGAGGAAATGTATGATACAC 183
Db 356 CAAGAAATACGGTCTTGCTATGAGATTTAGTAGCAGTAGAGGAAATGTATGATACAC 415
Qy 184 TTACGTTTGTGATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
Db 416 TTACGTTTGTGATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 475
Qy 244 TTGTAGAGTTGAGAAACCCAGTGTAGAACTATATTAGGGGCTGTTGTTGCTGTTA 303
Db 476 TTGTAGAGTTGAGAAACCCAGTGTAGAACTATATTAGGGGCTGTTGTTGCTGTTA 535
Qy 304 CTGTACACAGGAAACAGATTTCTTAAGGAAATCAAAATTAGGATAAGATTTCTATCTGATG 363
Db 536 CTGTACACAGGAAACAGATTTCTTAAGGAAATCAAAATTAGGATAAGATTTCTATCTGATG 595
Qy 364 AATATTTCCTTCTGAAACAGGGTTCTGCATCCATCAACATGTCTATGCCAATTTCA 423
Db 596 AATATTTCCTTCTGAAACAGGGTTCTGCATCCATCAACATGTCTATGCCAATTTCA 655
Qy 424 CAGAGCTGTGAGTCTCTCAGTGTACCCCTTTCAGCTTTCAGCTGAGCTGCTTAATA 483
Db 656 CAGAGCTGTGAGTCTCTCAGTGTACCCCTTTCAGCTTTCAGCTGAGCTGCTTAATA 715

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Qy 484 ATGCTATAACTGCCTTTAGTACTCTTGGAGACCTTATTTCGATATCTTGAACACAGAGAT 543
Db 716 ATGCTATAACTGCCTTTAGTACTCTTGGAGACCTTATTTCGATATCTTGAACACAGAGAT 775
Qy 544 GGCAGTTTGACATTTAGAAGATCTATATAGGCCAACTTTGGCAAATCTTCTTGGCAAGGCTTTTG 603
Db 776 GGCAGTTTGACATTTAGAAGATCTATATAGGCCAACTTTGGCAAATCTTCTTGGCAAGGCTTTTG 835
Qy 604 TTTTGGAAAGAAAATCCAGAGTGTGGATCTGAACCTTCTTAACAGAGGAGGTAAAGTTAT 563
Db 836 TTTTGGAAAGAAAATCCAGAGTGTGGATCTGAACCTTCTTAACAGAGGAGGTAAAGTTAT 895
Qy 664 ACAGCTGCACACCTCTGTAATCTCTAGTCTCCATAGGGAAGAACTTAAAGAGAACCCGATA 723
Db 896 ACAGCTGCACACCTCTGTAATCTCTAGTCTCCATAGGGAAGAACTTAAAGAGAACCCGATA 955
Qy 724 CCATTTCTGGCCAGGTTCTCTCTGGTTTAAACGCTGTGGTGGAACTGTGCTGTGTC 783
Db 956 CCATTTCTGGCCAGGTTCTCTCTGGTTTAAACGCTGTGGTGGAACTGTGCTGTGTC 1015
Qy 784 TCCACAATTTGCAATGAATCTCAATGTCTCCAGCAAAAGTTTACTAAATAATACCAGAG 843
Db 1016 TCCACAATTTGCAATGAATCTCAATGTCTCCAGCAAAAGTTTACTAAATAATACCAGAG 1075
Qy 844 TCCTTCAGTTTGAGACCAAAASACCGGTGTTCAGGGGATTGCAACAAATCACTCACCGAGCTGG 903
Db 1076 TCCTTCAGTTTGAGACCAAAAGACCGGTGTTCAGGGGATTGCAACAAATCACTCACCGAGCTGG 1135
Qy 904 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGACACAGAGAGTAGCCGC 963
Db 1136 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGACACAGAGAGTAGCCGC 1195
Qy 964 ATCAACACAGACAGCTCTTGCCAGAGCTGTGCAAGTGTGCTGATTTCTATTAGAGAA 1023
Db 1196 ATCAACACAGACAGCTCTTGCCAGAGCTGTGCAAGTGTGCTGATTTCTATTAGAGAA 1255
Qy 1024 CGTATCGGTTATCTCCATCTTAATCTCAGTTGTTTGTCTTCAAGGACCTTTTCACTCTCAG 1083
Db 1256 CGTATCGGTTATCTCCATCTTAATCTCAGTTGTTTGTCTTCAAGGACCTTTTCACTCTCAG 1315
Qy 1084 GATTTACAGTGCATCTGTAAGAGGAGACATCAACAGAGATTAGGAGTTGTGCAACAGCT 1143
Db 1316 GATTTACAGTGCATCTGTAAGAGGAGACATCAACAGAGATTAGGAGTTGTGCAACAGCT 1375
Qy 1144 CTTTGGAGGAGGCGCTTAAAGGACAGGAGAAAGGTCTTCAATCGTGGAAAGAAAATTAA 1203
Db 1376 CTTTGGAGGAGGCGCTTAAAGGACAGGAGAAAGGTCTTCAATCGTGGAAAGAAAATTAA 1435
Qy 1204 ATGTTGTATTAAATAGATCACAGCTAGTTTCAAGTTCACATGTACGTATTCCTAGC 1263
Db 1436 ATGTTGTATTAAATAGATCACAGCTAGTTTCAAGTTCACATGTACGTATTCCTAGC 1495
Qy 1264 TGGGTTCTGTATTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCAAGTACAGGAAAAAA 1323
Db 1496 TGGGTTCTGTATTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCAAGTACAGGAAAAAA 1555
Qy 1324 CTGTGCAAGTGTAGCACCTGATTCGGTTGCTTGTCTTAACTCTAAAGCTCCATGTCTCGG 1383
Db 1556 CTGTGCAAGTGTAGCACCTGATTCGGTTGCTTGTCTTAACTCTAAAGCTCCATGTCTCGG 1615
Qy 1384 CCTAAATCGTATAAAATCTGGA-TTTTTTTTTTTTTTTTTTTTTTCTCATATTCACATATGTA 1442
Db 1616 CCTAAATCGTATAAAATCTGGA-TTTTTTTTTTTTTTTTTTTTTTCTCATATTCACATATGTA 1675
Qy 1443 AACGAGAACATTTCTATGTACTACAAACCTGGTTTTTAAAGAGGAACTATGTTGCTATGAA 1502
Db 1676 AACGAGAACATTTCTATGTACTACAAACCTGGTTTTTAAAGAGGAACTATGTTGCTATGAA 1735
Qy 1503 TTAACCTTGTGTCATGCTGATAGGA 1527
Db 1736 TTAACCTTGTGTCATGCTGATAGGA 1760

```

RESULT 8

US-09-876-813-32
 ; Sequence 32. Application US/09876813
 ; GENERAL INFORMATION:
 ; APPLICANT: Gilbert, Teresa
 ; APPLICANT: Hart, Charles E.
 ; APPLICANT: Sheppard, Paul O.
 ; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
 ; FILE REFERENCE: 99-19
 ; CURRENT APPLICATION NUMBER: US/09/876,813
 ; CURRENT FILING DATE: 2001-06-06
 ; PRIOR APPLICATION NUMBER: US/09/564,595
 ; PRIOR FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: US 09/304,216
 ; PRIOR FILING DATE: 1999-05-03
 ; PRIOR APPLICATION NUMBER: US 60/164,463
 ; PRIOR FILING DATE: 1999-11-10
 ; PRIOR APPLICATION NUMBER: US 60/180,169
 ; PRIOR FILING DATE: 2000-02-04
 ; NUMBER OF SEQ ID NOS: 57
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 32
 ; LENGTH: 1760
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (154)...(1191)
 US-09-876-813-32

Query Match 98.4%; Score 1511; DB 5; Length 1760;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1522; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY	4	GTAAATTCAGTTTCCAGCAACAGGACAGACGGAGTACAGATCCTCAGCATGAGA	63
DB	236	GTAAATTCAGTTTCCAGCAACAGGACAGACGGAGTACAGATCCTCAGCATGAGA	295
QY	64	GAATTAATTAAGTCTGCTACTAATGAAGTATTACAGGCCCAAGTTTCTCATACTTATC	123
DB	296	GAATTAATTAAGTCTGCTACTAATGAAGTATTACAGGCCCAAGTTTCTCATACTTATC	355
QY	124	CAAGAAATACGCTCTGTGTAGGAGATTAGTAGGAGTACAGGAAATGTATGGATACAC	183
DB	356	CAAGAAATACGCTCTGTGTAGGAGATTAGTAGGAGTACAGGAAATGTATGGATACAC	415
QY	184	TTACGTTTGAATGAAGATTGGGCTTGAAGACCCAGAAAGATGACATATGCCAAGTATGAT	243
DB	416	TTACGTTTGAATGAAGATTGGGCTTGAAGACCCAGAAAGTACATATGCCAAGTATGAT	475
QY	244	TTGTAGAAGTTGAGAACCCAGTGAATGAACTATATAGGGCGCTGGTGTCTGGTA	303
DB	476	TTGTAGAAGTTGAGAACCCAGTGAATGAACTATATAGGGCGCTGGTGTCTGGTA	535
QY	304	CTGTACCCAGGAAACAGATTCTTAAAGGAAATCAAATTAGGATAAGATTGTATCTGATG	363
DB	536	CTGTACCCAGGAAACAGATTCTTAAAGGAAATCAAATTAGGATAAGATTGTATCTGATG	595
QY	364	AATATTTTCTGTAACAGAGGTTCTGCATCCATACAAATGTCTATGCCACAAATPCA	423
DB	596	AATATTTTCTGTAACAGAGGTTCTGCATCCATACAAATGTCTATGCCACAAATPCA	655
QY	424	CAGAGCTGTGAGTCTCTCAGTGTACCCCTTACGCTTTCAGCTTTCGACCTGCTTAATA	483
DB	656	CAGAGCTGTGAGTCTCTCAGTGTACCCCTTACGCTTTCGACCTGCTTAATA	715
QY	484	ATGCTATAACTGCTTTAGTACTTGGAGACCTTATTCGATATCTTGAACACAGAGAT	543
DB	716	ATGCTATAACTGCTTTAGTACTTGGAGACCTTATTCGATATCTTGAACACAGAGAT	775
QY	544	GGCAGTTGCACTAGAGATCTATATAGCCCACTTGGCACTTCTTGGCAAGGCTTTTG	603

DB	776	GGCAGTTGCACTTAGAGATCTATATAGCCCACTTGGCAACTTCTTGGCAGGCTTTTG	835
QY	604	TTTTTGGAGAAAAATCCAGAGTGGTGGATCTGAACTTCTTAAACAGAGGAGTAAATAT	663
DB	836	TTTTTGGAGAAAAATCCAGAGTGGTGGATCTGAACTTCTTAAACAGAGGAGTAAATAT	895
QY	664	ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGAGAACTTAAAGAGAACCGATA	723
DB	896	ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAGGAGAACTTAAAGAGAACCGATA	955
QY	724	CCATTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTGGTGGAACTGTCTGTGTGTC	783
DB	956	CCATTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTGGTGGAACTGTCTGTGTGTC	1015
QY	784	TCCAGAAATTTGCAATGCAATGTCAATGTGTCCCAAGCAAAAGTTACTTAAATAACACGAGG	843
DB	1016	TCCAGAAATTTGCAATGCAATGTCAATGTGTGTCCCAAGCAAAAGTTACTTAAATAACACGAGG	1075
QY	844	TCCTTCAGTTTGAGACCAAAACCCGGTGTCCAGGGGATTGCACAAATCACTCACCGACGTGG	903
DB	1076	TCCTTCAGTTTGAGACCAAAACCCGGTGTCCAGGGGATTGCACAAATCACTCACCGACGTGG	1135
QY	904	CCCTGAGACCAATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGAGGATAGCCGC	963
DB	1136	CCCTGAGACCAATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGAGGATAGCCGC	1195
QY	964	ATCACCAACAGCAGCTCTTCCCGCAGAGCTGTGCAGTCAGCTGCTGATTTCTATTAGAGAA	1023
DB	1196	ATCACCAACAGCAGCTCTTCCCGCAGAGCTGTGCAGTCAGCTGCTGATTTCTATTAGAGAA	1255
QY	1024	CGTATCGTTATCTCCATCTTAATCTCAGTTGTGTTGCTTCAAGGACCTTTTCATCTTCAG	1083
DB	1256	CGTATCGTTATCTCCATCTTAATCTCAGTTGTGTTGCTTCAAGGACCTTTTCATCTTCAG	1315
QY	1084	GATTTACAGTGCATCTGTAAGAGGAGACATCAACACAGAAATAGGAGTTGTGCAACAGCT	1143
DB	1316	GATTTACAGTGCATCTGTAAGAGGAGACATCAACACAGAAATAGGAGTTGTGCAACAGCT	1375
QY	1144	CTTTTGAGAGGAGCCCTAAAGGACAGGAGAAAGGCTCTTCAATCGTGGAAAGAAATTA	1203
DB	1376	CTTTTGAGAGGAGCCCTAAAGGACAGGAGAAAGGCTCTTCAATCGTGGAAAGAAATTA	1435
QY	1204	ATCTTGTATTAATAGATCACCAGCTAGTTTTCAGAGTTTACCATGTACGTTATTCCTAGC	1263
DB	1436	ATCTTGTATTAATAGATCACCAGCTAGTTTTCAGAGTTTACCATGTACGTTATTCCTAGC	1495
QY	1264	TGGGTTCTGTATTTTCACTTCTTCGATACGGCTTAGGGTAAATGTCTAGTACAGGAAAAA	1323
DB	1496	TGGGTTCTGTATTTTCACTTCTTCGATACGGCTTAGGGTAAATGTCTAGTACAGGAAAAA	1555
QY	1324	CTGTGCAAGTACAGCTGATTCGGTTGCTTAACTCTTAAAGCTCCATGTCTCTGGG	1383
DB	1556	CTGTGCAAGTACAGCTGATTCGGTTGCTTAACTCTTAAAGCTCCATGTCTCTGGG	1615
QY	1384	CCTAAATTCGTATAAAATCTGGA-TTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTA	1442
DB	1616	CCTAAATTCGTATAAAATCTGGA-TTTTTTTTTTTTTTTTTTTGTCTCATATTCATATGTA	1675
QY	1443	AACAGAACATCTTATGTACTACAAACCTGGTTTTTAAAGAACTATGTGTGCTATGAA	1502
DB	1676	AACAGAACATCTTATGTACTACAAACCTGGTTTTTAAAGAACTATGTGTGCTATGAA	1735
QY	1503	TTAAACTTGTGTCTCATCTGATAGGA	1527
DB	1736	TTAAACTTGTGTCTCATCTGATAGGA	1760

RESULT 9
 US-10-664-432-1
 ; Sequence 1. Application US/10664432
 ; GENERAL INFORMATION:
 ; APPLICANT: Hart, Charles E.
 ; APPLICANT: Gilbertson, Debra G.


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; FEATURE:
; OTHER INFORMATION: Fused DNA
US-09-457-066-50

Query Match      62.2%; Score 955.6; DB 5; Length 1095;
Best Local Similarity 99.9%; Pred. No. 5.2e-293;
Matches 955; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTAAATTCAGTTTCCAGCAACAGGAAACAGACCGAGTCAAGATCCTCAGCATGAGA 63
Db 122 GTAAATTCAGTTTCCAGCAACAGGAAACAGACCGAGTCAAGATCCTCAGCATGAGA 181

QY 64 GAATATTACTGTGTCTACTAATGAAGTATTTCACAGCCCAAGGTTTCTCATCTTATC 123
Db 182 GAATATTACTGTGTCTACTAATGAAGTATTTCACAGCCCAAGGTTTCTCATCTTATC 241

QY 124 CAAGAAATACCGTCTTGTGTATGGAGATTAGTAGAGTAAAGTAAATGTATGGATACAC 183
Db 242 CAAGAAATACCGTCTTGTGTATGGAGATTAGTAGAGTAAAGTAAATGTATGGATACAC 301

QY 184 TTACGTTTGATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
Db 302 TTACGTTTGATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 361

QY 244 TTGTAGAGTTGAGAACCCAGTGTGAACTATATTAGGGCGCTGTGTCTGTGTA 303
Db 362 TTGTAGAGTTGAGAACCCAGTGTGAACTATATTAGGGCGCTGTGTCTGTGTA 421

QY 304 CTGTACAGGAAACAGATTTCTAAAGGAAATCAAATTTAGGATGAAGTTTGTATCTGATG 363
Db 422 CTGTACAGGAAACAGATTTCTAAAGGAAATCAAATTTAGGATGAAGTTTGTATCTGATG 481

QY 364 AATATTTTCCCTTGAACCCAGGTTCTGCTACTCCACTACAATGTCTATGCCACAATCA 423
Db 482 AATATTTTCCCTTGAACCCAGGTTCTGCTACTCCACTACAATGTCTATGCCACAATCA 541

QY 424 CAGAGCTGTGAGTCCCTCAGTGTACCCCTTTCAGCTTTCCTGCTGCTGCTTAAATA 483
Db 542 CAGAGCTGTGAGTCCCTCAGTGTACCCCTTTCAGCTTTCCTGCTGCTGCTTAAATA 601

QY 484 ATGCTATAACCTGCTTGTAGTACCTTGAAGACCTTATTCGATATCTTGAACCAAGAGAT 543
Db 602 ATGCTATAACCTGCTTGTAGTACCTTGAAGACCTTATTCGATATCTTGAACCAAGAGAT 661

QY 544 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCACTTCTTGGCAAGCTTTTG 603
Db 662 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCACTTCTTGGCAAGCTTTTG 721

QY 604 TTTTGTGAAGAAATCCAGAGTGTGTGATCTGACCTTCTAACAGAGGAGTAAAGATTAT 663
Db 722 TTTTGTGAAGAAATCCAGAGTGTGTGATCTGACCTTCTAACAGAGGAGTAAAGATTAT 781

QY 664 ACAGTGCACACCTCGTAATCTTCACTGTCCATAAGGGAAGAACTAAAGAGACCGATA 723
Db 782 ACAGTGCACACCTCGTAATCTTCACTGTCCATAAGGGAAGAACTAAAGAGACCGATA 841

QY 724 CCATTTTCTGGCAGGTTGTCTCTGCTTAAACGCTGTGTGGGAACTGTGCTGTGTGTC 783
Db 842 CCATTTTCTGGCAGGTTGTCTCTGCTTAAACGCTGTGTGGGAACTGTGCTGTGTGTC 901

QY 784 TCCCAATTTGCAATGAATGTCAATGTCTCCCAAGCAAGTTACTTAAABAAATACCAAGG 843
Db 902 TCCCAATTTGCAATGAATGTCAATGTCTCCCAAGCAAGTTACTTAAABAAATACCAAGG 961

QY 844 TCCTTCAGTTGAGACCAAAACCGGTTTCAGGGGATTCGCAAAATCACTCACCGACGTGG 903
Db 962 TCCTTCAGTTGAGACCAAAACCGGTTTCAGGGGATTCGCAAAATCACTCACCGACGTGG 1021

QY 904 CCTGGAGCACCATGAGGAGTGTGACTGTGTGTGTCAGAGGAGGACACAGGAGGATAG 959
Db 1022 CCTGGAGCACCATGAGGAGTGTGACTGTGTGTGTCAGAGGAGGACACAGGAGGATAG 1077
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RESULT 11
US-09-457-066-42
; Sequence 42, Application US/09457066
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVBGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 3571
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1049) ... (2086)
US-09-457-066-42

Query Match      46.9%; Score 721; DB 5; Length 3571;
Best Local Similarity 83.6%; Pred. No. 4.1e-218;
Matches 817; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 4 GTAAATTCAGTTTCCAGCAACAGGAAACAGACCGAGTCAAGATCCTCAGCATGAGA 63
Db 1131 GCAATTTGCACTTCTCCAGCGACAGGAAACAGACCGAGTCAAGATCCTCAGCATGAGA 1190

QY 64 GAATATTACTGTGTCTACTAATGAAGTATTTCACAGCCCAAGGTTTCTCATCTTATC 123
Db 1191 GAGTTGTCACTATATCTGTAATGGAGCATCCACAGCCCAAGTTTCTCATCTTATC 1250

QY 124 CAAGAAATACCGTCTTGTGTATGGAGATTAGTAGAGTAAAGTAAATGTGCGGATCCAGC 183
Db 1251 CAAGAAATACCGTCTTGTGTATGGAGATTAGTAGAGTAAAGTAAATGTGCGGATCCAGC 1310

QY 184 TTACGTTTGATGAAGATTTGGGCTTGAAGACCCAGAGATGACATATGCAAGTATGATT 243
Db 1311 TGACATTTGATGAGATTTGGGCTGGAAGATCCAGAGACGAATATGCAAGTATGATT 1370

QY 244 TTGTAGAGTTGAGAACCCAGTGTGAACTATATTAGGGCGCTGTGTGCTGTGTA 303
Db 1371 TTGTAGAGTTGAGAACCCAGTGTGAAAGTGTGTTAGGACGCTGTGTGCTGTGGA 1430

QY 304 CTGTACAGGAAACAGATTTCTAAAGGAAATCAAATTTAGGATGAAGTTTGTATCTGATG 363
Db 1431 CTGTACAGGAAACAGATTTCTAAAGGAAATCAAATTTAGGATGAAGTTTGTATCTGATG 1490

QY 364 AATATTTTCCCTTCTGAACCCAGGTTTCTGCTCACTCAACATTTGTCCAGCAATTC 423
Db 1491 AGTATTTTCCATCTGAACCCGATTTCTGCTCACTCACTACAGTATTTATCATGCCAAGTCA 1550

QY 424 CAGAGCTGTGAGTCTTCACTGTGTACCCCTTTCAGCTTTGCGCACTGGAAGTCTGTTAATA 483
Db 1551 CAGAGCTGTGAGTCTTCACTGTGTACCCCTTTCAGCTTTGCGCACTGGAAGTCTGTTAATA 1610

QY 484 ATGCTATAACTGCTTTTAGTACCTTGGAGACCTTATTCGATATCTTGAACCAAGAGAT 543
Db 1611 ATGCTGTGACTGCTTTTAGTACCTTGGAGACCTTATTCGATATCTTGAACCAAGAGAT 1670

QY 544 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCACTTCTTGGCAAGCTTTTG 603
Db 1671 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCACTTCTTGGCAAGCTTTTG 1730

QY 604 TTTTGTGAAGAAATCCAGAGTGTGTGATCTGAACTTCTTAAACAGAGGAGGTAAGATTAT 663
Db 1731 TGTATGGGAAAAAGGAAAGTGTGAAATCTGAAATCTCTCTCTCAAGGAAAGGTAAGAACTCT 1790
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QY 664 ACAGTGCACACCTCGTAACCTCTCAAGTGTCCATTAAGGAGAGAACTAAGAGAACCGATA 723
Db 1791 ACAGTGCACACCCCGAACTTCTCAGTGTCCATACCGGAGAGCTTAAAGAGGACAGATA 1850
QY 724 CCATTTCTGGCCAGGTGTCTCCTGGTTAAACGCTGTGGTGGAACTGTGCTGTGTGC 783
Db 1851 CCATTTCTGGCCAGGTGTCTCCTGGTCAAGGCTGTGGAGAAATTTGCTGTGTGC 1910
QY 784 TCACAAATTGCAATGAATGTCAATGTGTCCCAAGCAAGTTCATTAATAATACCAAGG 843
Db 1911 TCACAAATTGCAATGAATGTCAATGTGTCCCAAGTTCATTAATAATACCAAGG 1970
QY 844 TCCTTCAGTTGAGACCAAAACCGGTGTCAAGGGATTGACAAATCACTCACCGAGCTG 903
Db 1971 TCCTTCAGTTGAGACCAAAACCGGTGTCAAGGGATTGACAAATCACTCACCGAG 2030
QY 904 CCCTGGAGCACCATTGAGAGAGTGTGACTGTGTGTCAGAGGAGGACACAGAGGATACCCGC 963
Db 2031 CTCTGGAGCACCATTGAGAGAGTGTGACTGTGTGTCAGAGGAGGACACAGAGG 2090
QY 964 ATCACCACAGCAGCTC 980
Db 2091 AGCCTTCGTAGCAGCAC 2107

RESULT 12
US-09-876-813-34
; Sequence 34, Application US/09876813
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 3571
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1049)...(2086)
US-09-876-813-34

Query Match 46.9%; Score 721; DB 5; Length 3571;
Best Local Similarity 83.6%; Pred. No. 4.1e-218;
Matches 817; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 4 GTAAATTCAGTTTCCAGCAACAAAGGACAGAGACGAGTACAGATCCTCAGCATGAGA 63
Db 1131 GCAAGTTGCAGCTCTCCAGCAGCAGGACAGAGACGAGTCCAGATCCCGGATGAGA 1190
QY 64 GAAATTTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGTTTCTCCTCATCTATC 123
Db 1191 GAGTTGTCACTATATCTGGTAATGGAGCATCCACAGCCCAAGTTTCTCCTCATACATCC 1250
QY 124 CAAGAAATACGCTCTTGTGTATGGAGATTAGTAGCAGTAGAGGAAATGTGGATACAAC 183
Db 1251 CAAGAAATATGGTGTGTGTGGAGATTAGTTGAGTAGATGAAATGTGCGGATCCAGC 1310
QY 184 TTACGTTTGAAGAAGTTTGGGCTTGAAGACCCAGAGAGATGACATATGCAAGTATGATT 243

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Db 1311 TCACATTTGATGAGAGATTTTGGGCTGGAAGATCCAGAAGACGATATATGCAAGTATGATT 1370
QY 244 TTGTAGAAGTTGAGAGAACCCAGTGTATGGAACATATATTAGGCGGCTGTGTGTGTTGCTGTA 303
Db 1371 TTGTAGAAGTTTGAAGAGCCAGTGTATGGAAGTGTGTGTAGGACGCTGTGTGTGTTGCTGGA 1430
QY 304 CTGTACACAGGAAACACAGATTTCTAAAGGAAATCAAAATAGGATAAGATTGTGTATCTGATG 363
Db 1431 CTGTACACAGGAAACACAGATTTCTAAAGGAAATCAAAATAGGATAAGATTGTGTATCTGATG 1490
QY 364 AATATTTTCTTCTTGAAACCAAGGTTCTGCATCCACTCAACATTTGTGTCTATGCGCAAAATTC 423
Db 1491 AGTATTTTCTTCTTGAAACCAAGGTTCTGCATCCACTCAACATTTGTGTCTATGCGCAAAATTC 1550
QY 424 CAGAGCTGTGAGTCTTCTCAGTGTCTACCCCTTCCAGCTTTGCCACTGACCTGCTTAAATA 483
Db 1551 CAGAAACCAAGTCTTCTGCGTGTGTGCGCTTCTATCTTTGTCTATGCGCAAAATTCCTCAACA 1610
QY 484 ATGCTATTAACCTGCTTTAGTACCTTTGGAAGACCTTTATTCGATATCTTGAACCAAGAGAT 543
Db 1611 ATGCTGTGACTGCTTTAGTACCTTTGGAAGAGCTGATTGCGGTACCTAGAGCCAGATCGAT 1670
QY 544 GGCAGTTGGAATTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG 603
Db 1671 GGCAGTTGGAATTAGAAGATCTATATAGGCCAACTTGGCAAGGCTTTTG 1730
QY 604 TTTTGGAAAGAAATCCAGAGTGGTGGATCTGAACCTTTCTAACAGAGGAGGTAAAGATTAT 663
Db 1731 TGTATGGGAAAGAAAGCAAGTGGTGAATCTGAATCTCTCTCAAGGAAGAGGTAAAGCTCT 1790
QY 664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA 723
Db 1791 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA 1850
QY 724 CCATTTCTGGCCAGGTTGTCTCTGCTGTAAACGCTGTGTGGAACTGTGCTCTGTGTC 783
Db 1851 CCATTTCTGGCCAGGTTGTCTCTGCTGTAAACGCTGTGTGGAACTGTGCTCTGTGTC 1910
QY 784 TCCCAAAATTCGAATGAATGTCTCAATGTGTGCCCAAGCAAAAGTTTACTAAAAAATACCAAGG 843
Db 1911 TCCCAAAATTCGAATGAATGTCTCAATGTGTGCCCAAGCAAAAGTTTACTAAAAAATACCAAGG 1970
QY 844 TCCTTCAGTTGAGACCAAAACCGGTGTGTCAGGGGATTCACAAATCACTCACCGAGCTGG 903
Db 1971 TCCTTCAGTTGAGACCAAAACCGGTGTGTCAGGGGATTCACAAATCACTCACCTGATGTTG 2030
QY 904 CCCTGGAGCACCATTGAGAGTGTGACTGTGTGTCAGAGGAGGACACAGAGGATAGCCGC 963
Db 2031 CTCTGGAGCACCATTGAGAGTGTGACTGTGTGTCAGAGGAGGACACAGAGGATAGCCGC 2090
QY 964 ATCACCACAGCAGCTC 980
Db 2091 AGCCTTCGTAGCAGCAC 2107

RESULT 13
US-10-664-432-3
; Sequence 3, Application US/10664432
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/10/664,432
; CURRENT FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: Mus musculus

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/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1049) ... (2086)
US-10-664-432-3

Query Match 46.9%; Score 721; DB 6; Length 3571;
Best Local Similarity 83.6%; Pred. No. 4.1e-218;
Matches 817; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

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QY 4 GTAAATTCAGTTTTCAGCAACAAAGAAACAGACCGAGTACAAAGATCCTCAGCATGAGA 63
Db 1131 GCAAGTTGAGCTCTCCAGCGACAGAGAAAGAGAGAGTCCCGGCAATGAGA 1190
QY 64 GAATTATCTGTCTCTAATGGAAGTATTCACAGCCCAAGTTTCCTCATCTATTC 123
Db 1191 GAGTTGTCTATATCTGTGTAATGGAGCATCCACAGCCCGAAGTTTCCTCATACATCC 1250
QY 124 CAAGAATACGCTCTGGTATGAGATTTAGCAGTAGGAGAAATGTATGATACAC 183
Db 1251 CAAGAATATGGTCTGGTATGAGATTTAGTGGATGATGAAATGTGCGGATCCAGC 1310
QY 184 TTACGTTTGATGAAGATTTGGGCTTGAGACCCAGAAAGATGACATATGCAAGTATGATT 243
Db 1311 TGACATTTGATGAGATTTGGGCTGGAAGATCCAGAGACGATATATGCAAGTATGATT 1370
QY 244 TTGTAGAGTTGAGGAACCCAGTGTGGAACATATATAGGGCGTGGTGTCTGGTA 303
Db 1371 TTGTAGAGTTGAGGAACCCAGTGTGGAAGTGTGTTAGGACGCTGGTGTCTGGGA 1430
QY 304 CTGTACAGGAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGATCTGATG 363
Db 1431 CTGTGCGAGGAAGAGAGATTTCTAAAGGAAATCATATCAGGATAAGATTTGATCTGATG 1490
QY 364 AATATTTTCTCTGAAACAGGTTCTGCATCCACTACAAATGTCATGCCCAATTC 423
Db 1491 AGTATTTTCCATCTGAACCCGATTTCTGCATCCACTACAGTATATATGCGCAAGTCA 1550
QY 424 CAGAAGCTGTGAGTCTCTAGTCTACCCCTTACGTTTGGCACTGGACCTGCTTAATA 483
Db 1551 CAGAAACACAGAGTCTCTGGTGTGCGCCCTTATCTGTCATTTGGACCTGCTCAACA 1610
QY 484 ATGCTATAACTGCTTTAGTACCTTGGAGAGACCTTATTCGATATCTTGAACAGAGAGAT 543
Db 1611 ATGCTGTGACTGCTTTCAGTACCTTGGAGAGCTGATTCGGTACCTAGAGCCAGATCGAT 1670
QY 544 GGCAGTTGACCTTAGAAGATCTATATAGGCCAACTTTGGCAACTTTTGGCAAGGCTTTTG 603
Db 1671 GGCAGTTGACCTTAGACAGCTCTACAAGCCAACTATGGCAGCTTTTGGCAAGGCTTTTC 1730
QY 604 TTTTGGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGTAAAGATTAT 663
Db 1731 TGTATGGGAAGAAAGCAAGTGGTGAATCTGAATCTCTCTCAAGGAAGAGGTAAACTCT 1790
QY 664 ACAGCTGCACTCTGTAATCTTCTAGTGTCCATAAGGGAAGAACTTAAAGAGAACCGATA 723
Db 1791 ACAGCTGCACTCCCGGAATCTCAGTGTCCATACGGAAGAGCTTAAAGAGACAGATA 1850
QY 724 CCATTTCTGCGCAGGTTGCTCTGGTTAAAGCTGTGGTGGAACTCTGTGCTGTGTGTC 783
Db 1851 CCATATTTGCGCAGGTTGCTCTGGTCAAGCGCTGTGGAGAAATTTGTGCTGTGTGTC 1910
QY 784 TCCAAATTTGCAATGATGATCTAATGTCTCCAGCAAGTTACTTAAATAATACCCAGG 843
Db 1911 TCCATTAATTTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1970
QY 844 TCTTCAGTTGAGACCAASACCGGTGTGTCAGGGGATTTGACAAATCACTCACCGAGTGG 903
Db 1971 TCTTCAGTTGAGACCAASACCGGTGTGTCAGGGGATTTGATAGTCACTCACTGATGTCG 2030
QY 904 CCTGGAGCACCATGAGGAGTGTGCTGTGTGTCAGAGGGAGCAAGAGGATAGCCGC 963
Db 2031 CTCTGGAACACACGAGGAATGATGCTGTGTGTGTAGAGGAAACGAGGAGGTAACTGC 2090
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QY 964 ATCACCAACAGCAGCTC 980
Db 2091 AGCCTTCGTAGCAGCAC 2107
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RESULT 14

US-60-487-610-19346
; Sequence 19346, Application US/60487610
; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19346

; LENGTH: 221510
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: misc_feature
; LOCATION: (1) ... (221510)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1

US-60-487-610-19346

Query Match 45.2%; Score 694.4; DB 7; Length 221510;
Best Local Similarity 97.8%; Pred. No. 1.1e-208;
Matches 698; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

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QY 823 TTAATAAAATACCAACGAGTCTTCAGTTGAGACCAACCGGTGTCAGGGATTGC 882
Db 213895 TTAATCTTATCCCTTTCAGTTCAGTTGAGACCAACCGGTGTCAGGGATTGC 213954
QY 883 ACAATATCACTACCGAGTGGCCCTGGAGCACCATGAGAGTGTGACTGTGTGCGAGAG 942
Db 213955 ACAATATCACTACCGAGTGGCCCTGGAGCACCATGAGAGTGTGACTGTGTGCGAGAG 214014
QY 943 GGAGCACAGAGGATAGCGCATCAACACAGCAGCTCTTGGCCAGAGCTGTGCGATGCA 1002
Db 214015 GGAGCACAGGAGATAGCGCATCAACACAGCAGCTCTTGGCCAGAGCTGTGCGATGCA 214074
QY 1003 GTGGCTGATTTCTATTAGAGAGCTATGCTTATCCATCCTTAATCTCAGTTGTTGCT 1062
Db 214075 GTGGCTGATTTCTATTAGAGACRTATGCGTTATCTCCATCTTAATCTCAGTTGTTGCT 214134
QY 1063 TCAAGGACCTTTTCATCTTCAGGATTTTACAGTGCATTTCTGAAAGAGAGACATCAAAACAGA 1122
Db 214135 TCAAGGACCTTTTCATCTTCAGGATTTTACAGTGCATTTCTGAAAGAGAGACATCAAAACAGA 214194
QY 1123 ATTAGAGTGTGCAACAGCTCTTTTGAGAGAGGCTTAAAGACAGGAGAAAAGTCTTT 1182
Db 214195 ATTAGAGTGTGCAACAGCTCTTTTGAGAGAGGCTTAAAGACAGGAGAAAAGTCTTT 214254
QY 1183 CAATCGTGAAGAAAATTAATGTTGATTAATAAGATCACCAGCTAGTTTCAGAGTTA 1242
Db 214255 CAATCGTGAAGAAAATTAATGTTGATTAATAAGATCACCAGCTAGTTTCAGAGTTA 214314
QY 1243 CCATGTAGCTATTCATAGCTGGGTTCGTATTTTTCAGTTCTTTTCATACCGCTTAGGGT 1302
Db 214315 CCATGTAGCTATTCATAGCTGGGTTCGTATTTTTCAGTTCTTTTCATACCGCTTAGGGT 214374
QY 1303 ATGTGAGTACAGGAAAAAACTGTGCAAGTGAACCTGATCCGTTGCCCTTGTCTAAC 1362
Db 214375 ATGTGAGTACAGGAAAAAACTGTGCAAGTGAACCTGATCCGTTGCCCTTGTCTAAC 214434
QY 1363 TCTAAAGCTCCATGTCTCGGGCTAAATCGTATAAATCTGATTTTTTTTTTTTTTTTTT 1422
Db 214435 TCTAAAGCTCCATGTCTCGGGCTAAATCGTATAAATCTGATTTTTTTTTTTTTTTTTT 214494
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QY      1423  TCGTCATATTACATATGTAACACGAGCAATTCATGTACTACAAACCTGGTTTTAAAA 1482
Db      214495  TCGTCATATTACATATGTAACACGAGCAATTCATGTACTACAAACCTGGTTTTAAAA 214554

QY      1483  AGGAACATGTGGCTATGAATTAACCTTGTGTCATGCTGATAGGACAGACTGGA 1536
Db      214555  AGGAACATGTGGCTATGAATTAACCTTGTGTCATGCTGATAGGACAGACTGGA 214608

RESULT 15
US-60-485-450-11913
; Sequence 11913, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-tung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11913
; LENGTH: 221510
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(221510)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Ta
US-60-485-450-11913

```

Query Match	45.2%	Score 694.4	DB 7	Length 221510
Best Local Similarity	97.8%	Pred. No. 1.1e-208		
Matches 698	Conservative 5	Mismatches 11	Indels 0	Gaps 0
QY	823	TTACTAAAAATACACAGAGTCCCTTCAGTTTGAGACCAAAACCGGTGTTCAGGGGATTGC	882	
Db	213895	TTACTCTTATTCCTTTTCAGGTCCCTTCAGTTTGAGACCAAAACCGGTGTTCAGGGGATTGC	213954	
QY	883	ACAAATCACTCACCGAAGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGCAGAG	942	
Db	213955	ACAAATCACTCACCGAAGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGCAGAG	214014	
QY	943	GGAGCAGGAGGATAGCCGCATACCAACGACGACTCTTGCCACAGAGCTGTGCAGTGCA	1002	
Db	214015	GGAGCAGGAGGATAGCCGCATACCAACGACGACTCTTGCCACAGAGCTGTGCAGTGCA	214074	
QY	1003	GTGCTGATTCCTATTAGAGACGATGCGTTATCTCCATCCTTAATCTCAGTTGTTGCT	1062	
Db	214075	GTGCTGATTCCTATTAGAGACGATGCGTTATCTCCATCCTTAATCTCAGTTGTTGCT	214134	
QY	1063	TCAAGGACCTTTCATCTTTCAGGATTTACAGTGCATTTCTGAAAGAGGAGACATCAACAGA	1122	
Db	214135	TCAAGGACCTTTCATCTTTCAGGATTTACAGTGCATTTCTGAAAGAGGAGACATCAACAGA	214194	
QY	1123	ATTAGAGTTGTGCAACAGCTCTTTTGTAGAGAGCGCTTAAAGGACAGAGAAAAGGCTTT	1182	
Db	214195	ATTAGAGTTGTGCAACAGCTCTTTTGTAGAGAGCGCTTAAAGGACAGAGAAAAGGCTTT	214254	
QY	1183	CAATCGTGGAAAGAAAATTAAGTTGTATTAAATAGATCACACGTAGTTTCACAGTTA	1242	
Db	214255	CAATCGTGGAAAGAAAATTAAGTTGTATTAAATAGATCACACGTAGTTTCACAGTTA	214314	
QY	1243	CCATGTAGCTATTCACACTAGCTGGGTTCGTATTTCAGTTCTTTCCGATACGGCTTAGGGT	1302	
Db	214315	CCATGTAGCTATTCACACTAGCTGGGTTCGTATTTCAGTTCTTTCCGATACGGCTTAGGGT	214374	
QY	1303	AATGTCAGTACAGGAAAAAAACTGTGCAAGTGAGCACTGATTCGGTTCGCTTGTAAAC	1362	
Db	214375	AATGTCAGTACAGGAAAAAAACTGTGCAAGTGAGCACTGATTCGGTTCGCTTGTAAAC	214434	

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 25, 2003, 23:39:26 ; Search time 2241.28 Seconds
(without alignments)
16656.442 Million cell updates/sec

Title: US-09-852-209A-4

Perfect score: 1536

Sequence: 1 cgggtaaatccagttttcc.....tgctgtaggacagactgga 1536

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hcc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estom:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_fod:*
26: em_gss_ptg:*
27: em_gss_vrt:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1484.8	96.7	2826	11	BC041783
2	1481.4	96.4	2655	11	BC051876
3	787.2	51.3	999	13	BQ068266
4	779.6	50.8	969	10	BG677432

5	767.6	50.0	811	10	BG185961
6	758.8	49.4	1142	10	BG681390
7	733	47.7	802	12	BI870535
8	721	46.9	2765	11	AK052947
9	721	46.9	3244	11	AK033734
10	721	46.9	3405	11	AK042767
11	696.8	45.4	769	14	CB309471
12	693.8	45.2	2893	11	BC029099
13	640	41.7	686	12	BQ015321
14	604.2	39.3	2502	11	AK081347
15	572.4	37.3	789	12	BI911795
16	568	37.0	572	13	BQ694737
17	519.8	33.8	696	10	BG430400
18	489.4	31.9	567	12	BM827309
19	489.2	31.8	823	13	BU614825
20	489	31.8	500	10	BE326924
21	481.8	31.4	523	10	BE958470
22	481.4	31.3	982	13	BU459467
23	478.4	31.1	851	10	BF102859
24	478.2	31.1	950	10	BF031624
25	477.6	31.1	902	13	BU517879
26	473.8	30.8	820	10	BF697294
27	473	30.8	874	10	BF670092
28	466.4	30.4	676	13	BU259419
29	465.8	30.3	565	10	BE884591
30	456	29.7	695	12	BI668022
31	443.6	28.9	556	10	BG609411
32	432.2	28.1	877	10	BF137533
33	431	28.1	477	14	CB159806
34	411.4	26.8	559	12	BM053696
35	411	26.8	412	14	W21436
36	408	26.6	425	9	AA759138
37	407.8	26.5	564	10	BF151355
38	407.4	26.5	889	10	BF698737
39	401.4	26.1	983	10	BG112388
40	387	25.2	562	9	AU280428
41	386.8	25.2	764	10	BF541705
42	384.4	25.0	523	10	BF021679
43	378.8	24.7	511	9	AW210331
44	378.6	24.6	968	10	BG118707
45	374.6	24.4	618	10	BG221261

ALIGNMENTS

RESULT 1
BC041783

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

BC041783 2826 bp mRNA linear HTC 13-JAN-2003
Homo sapiens, Similar to platelet-derived growth factor, C
polypeptide, clone IMAGE:461450, mRNA.

BC041783.1 GI:27692870

HTC.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 2826)

Strausberg, R.

Direct Submission

Submitted (23-DEC-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapsb-f@mail.nih.gov

Tissue Procurement: CLONTECH

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)

RNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

BG185961 RST4916 A
BG681390 602627750
BI870535 603394005
AK052947 Mus muscu
AK033734 Mus muscu
AK042767 Mus muscu
CB309471 AGENCOURT
BC029099 Mus muscu
BQ015321 UI-H-ED1-
AK081347 Mus muscu
BF911795 603065222
BQ694737 1000880 H
BG430400 602502113
BM827309 K-EST0099
BU614825 UI-M-EV0-
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BU459467 603368015
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BF031624 601558104
BU517879 AGENCOURT
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BF670092 602119417
BU259419 603415593
BE884591 601506290
BI668022 603295848
BG609411 323251 MA
BF137533 601780532
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BG112388 602281957
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BF541705 602068532
BF021679 uy50f05.Y
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BG221261 RST41064